



```

Db 181 STLTMLPLCGNCCIDHFFCEPLINQLACVDTSLNEMEMYLASFVVLPLGLILSVG 240
QY 241 HIARAVLKIRSAEGRKANTCSSHVAVVSLFVGSIIIFMYLQPAKSTSHSQGKFTALPYT 300
Db 241 HIARAVLKIRSAEGRKANTCSSHVAVVSLFVGSIIIFMYLQPAKSTSHSQGKFTALPYT 300
QY 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340
Db 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340

RESULT 2
O2C3_HUMAN
ID O2C3_HUMAN STANDARD; PRT; 319 AA.
AC Q8NGW7; Q8NGW7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Olfactory receptor 2C3.
GN Name=OR2C3; Synonyms=OR2C4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubumi S., Aburatani H., Asai K., Akiyama Y.
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins P.S., Wagner L., Schenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Exploatorium
CC (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB065649; BAC05875.1; ALT_INIT.
CC EMBL; BC030717; AAH30717.1;

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Genew: HGNC:15005; OR2C3.
InterPro: IPR000276; GPCR_Rhodpsn.
InterPro: IPR000725; Olfact_receptor.
Pfam: PF00001; 7tm_1; 1.
PRINTS: PR00237; GPCR_Rhodopsin.
PRINTS: PR00245; OLFACTORYR.
PROSITE: PS00237; G PROTEIN RECP FL 1; 1.
PROSITE: PS00262; G PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Transmembrane.
FT DOMAIN 1 25 Extracellular (Potential).
FT TRANSMEM 26 49 1 (Potential).
FT DOMAIN 50 57 Cytoplasmic (Potential).
FT TRANSMEM 58 79 2 (Potential).
FT DOMAIN 80 100 Extracellular (Potential).
FT TRANSMEM 101 120 3 (Potential).
FT DOMAIN 121 139 Cytoplasmic (Potential).
FT TRANSMEM 140 158 4 (Potential).
FT DOMAIN 159 195 Extracellular (Potential).
FT TRANSMEM 196 219 5 (Potential).
FT DOMAIN 220 236 Cytoplasmic (Potential).
FT TRANSMEM 237 259 6 (Potential).
FT DOMAIN 260 272 Extracellular (Potential).
FT TRANSMEM 273 292 7 (Potential).
FT DOMAIN 293 319 Cytoplasmic (Potential).
FT DISULFID 97 189 By similarity.
FT CARBOHYD 5 5 N-linked (GlcNAc...) (Potential).
FT CONFLICT 13 19 A -> T (in Ref. 1).
FT CONFLICT 67 67 S -> P (in Ref. 1).
SQ SEQUENCE 319 AA; 35204 MW; C1433C539904DB19 CRC64;

Query Match 92.8%; Score 1649; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 3, 7e-116;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 MEIANVSSPEVFLVGLGFSRPSLETVFLVLSFYVMSILGNGIILVSHSTDVHLTPMY 81
Db 1 MEIANVSSPEVFLVGLGFSRPSLETVFLVLSFYVMSILGNGIILVSHSTDVHLTPMY 60
QY 82 FFLANLSFLDMSFTTSIVPQLLANWGPKTTSYGGCVVQFVISHWLGATECVLLATMSY 141
Db 61 FFLANLSFLDMSFTTSIVPQLLANWGPKTTSYGGCVVQFVISHWLGATECVLLATMSY 120
QY 142 DRYAATCRPLHYTVIMHPQLCLGLALASWLGTLTSMVGSITLMLPLCGNCCIDHFFCE 201
Db 121 DRYAATCRPLHYTVIMHPQLCLGLALASWLGTLTSMVGSITLMLPLCGNCCIDHFFCE 180
QY 202 MPLIMQLACVDTSLNEMEMYLASFVVLPLGLILSVYGHIAVAVKIRSAEGRKAFNT 261
Db 181 MPLIMQLACVDTSLNEMEMYLASFVVLPLGLILSVYGHIAVAVKIRSAEGRKAFNT 240
QY 262 CSSHVAVVSLFYGSIIFMYLQPAKSTSHSQGKFTALPYTVTPALNPLIYTLRNTVEKSA 321
Db 241 CSSHVAVVSLFYGSIIFMYLQPAKSTSHSQGKFTALPYTVTPALNPLIYTLRNTVEKSA 300
QY 322 LRHMVLENCSSAGKLAQI 340
Db 301 LRHMVLENCSSAGKLAQI 319

RESULT 3
Q8VPHO PRELIMINARY; PRT; 317 AA.
ID Q8VPHO;
AC Q8VPHO;
DT 01-MAR-2002 (TRENDEL. 20, Created)
DT 01-MAR-2002 (TRENDEL. 20, Last sequence update)
DT 01-MAR-2004 (TRENDEL. 26, Last annotation update)
DE Olfactory receptor MOR256-12.
GN Name=Olfir361;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21676863; PubMed=11802173;
RA  Zhang X., Firestein S.;
RT  "The olfactory receptor gene superfamily of the mouse.";
RL  Nat. Neurosci. 5:124-133(2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21864069; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA  Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RT  Trask B.J.;
RL  "Different evolutionary processes shaped the mouse and human olfactory
  receptor gene families.";
RN  Hum. Mol. Genet. 11:535-546(2002).
RN  [3]
RP  SEQUENCE FROM N.A.
RA  Adams M.;
RL  Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY073556; AAL61219.1; -.
DR  MGD; MGI:3031195; Olfr1361.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004984; F:olfactory receptor activity; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR  Pfam; PF00001; 7tm.1; 1.
DR  PRINTS; PR00237; GPCR_RHODOPSIN.
DR  PROSITE; PS00245; OLFACTORYTR.
DR  PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR  PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW  Receptor.
SQ  SEQUENCE 317 AA; 35424 MW; 7DF0EF9EC7147B00 CRC64;

Query Match 56.8%; Score 1009; DB 2; Length 317;
Best Local Similarity 61.9%; Pred. No. 5.1e-69;
Matches 190; Conservative 51; Mismatches 64; Indels 2; Gaps 2;

Qy  21 MMEIANVSSPEVFLVGLGFSARPSLETVLFIVLVSYFVMSYILNGIILVSHVTDVHLHTPM 80
Db  5 VMKENTSSPEGFILVGFSDRPHLELILFVVVLSFYLLTLGNNTIILSALDSRLHTPM 64
Qy  81 YFFLANLSFLDMSPFTTSIVPOLLANLWGPQKTSISYGCVQVQFYISHWLGATECVLLATMS 140
Db  65 YFFLANLSFLDMCFITGSIPQMLYNLWGPDKTISYVGCALQLYFVALGGVECVLLAVMA 124
Qy  141 YDRAAICRPLHYTVIMHPOLCIGLALASWLGGLTTSWVGSTLTMLPLCGNCCIDHFFC 200
Db  125 YDRAAACKPLHYTVIMHPRLCGLASVAMLSGFGNSLIMAPQTLMLPRCGHRRVDHFLC 184
Qy  201 EMPLIMOLACVDT-SLNEMEMYLASFVFLVPLGLILVSYGHIAVARAVLKIRSAEGRKAF 259
Db  185 EMPALIGMACVDNMLEALAFALAFI-ILAPLILISYGIARAVFRKSAAGRRKAF 243
Qy  260 NTCSSHVAVVSLFYGSIFMYLQPAKSTSHSQKFIALFYTVVTPALNPLIYTLRNTEVK 319
Db  244 NTCSSHLIVVSLFYGTIIYVLPANTYSODQKFLTFYITVTPSNVPLIYTLRNKDKV 303
Qy  320 SALRHMV 326
Db  304 EAVKVL 310

RESULT 4
Q7TQU4 ID Q7TQU4 PRELIMINARY; PRT; 312 AA.
AC Q7TQU4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Olfactory receptor Olfr1361.
GN Name=Olfr1361;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Trask B.J.;
"Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and unequal
expression levels.";
Genome Biol. 4:R71-R71(2003).
[2]
SEQUENCE FROM N.A.
Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY318570; AAP71745.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodopsin.
Pfam; PF00001; 7tm.1; 1.
PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 312 AA; 34766 MW; 79B51A4BF642716A CRC64;

Query Match 56.8%; Score 1008; DB 2; Length 312;
Best Local Similarity 62.1%; Pred. No. 6e-68;
Matches 190; Conservative 50; Mismatches 64; Indels 2; Gaps 2;

Qy  22 MEIANVSSPEVFLVGLGFSARPSLETVLFIVLVSYFVMSYILNGIILVSHVTDVHLHTPM 81
Db  1 MEKENTSSPEGFILVGFSDRPHLELILFVVVLSFYLLTLGNNTIILSALDSRLHTPM 60
Qy  82 YFFLANLSFLDMSPFTTSIVPOLLANLWGPQKTSISYGCVQVQFYISHWLGATECVLLATMS 141
Db  61 YFFLANLSFLDMCFITGSIPQMLYNLWGPDKTISYVGCALQLYFVALGGVECVLLAVMA 120
Qy  142 DRYAAICRPLHYTVIMHPOLCIGLALASWLGGLTTSWVGSTLTMLPLCGNCCIDHFFC 201
Db  121 DRYAAACKPLHYTVIMHPRLCGLASVAMLSGFGNSLIMAPQTLMLPRCGHRRVDHFLC 180
Qy  202 MPLIMOLACVDT-SLNEMEMYLASFVFLVPLGLILVSYGHIAVARAVLKIRSAEGRKAF 260
Db  181 MPALIGMACVDNMLEALAFALAFI-ILAPLILISYGIARAVFRKSAAGRRKAF 239
Qy  261 TCSSHVAVVSLFYGSIFMYLQPAKSTSHSQKFIALFYTVVTPALNPLIYTLRNTEVKS 320
Db  240 TCSSHLIVVSLFYGTIIYVLPANTYSODQKFLTFYITVTPSNVPLIYTLRNKDKVE 299
Qy  321 ALRHMV 326
Db  300 AVKVL 305

RESULT 5
Q6IF45 ID Q6IF45 PRELIMINARY; PRT; 350 AA.
AC Q6IF45
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Olfactory receptor ORI-33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
PubMed=14983052; DOI=10.1073/pnas.0307882100;
Malnic B., Godfrey P.A., Buck L.B.;
"The human olfactory receptor gene family.";
Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).
```

CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -|- MISCELLANEOUS: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
 DR EMBL: BK004417; DAA04815.1; .  
 DR GO: GO:0016021; C: integral to membrane; IEA.  
 DR GO: GO:0004984; F: olfactory receptor activity; IEA.  
 DR GO: GO:0004872; F: receptor activity; IEA.  
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro: IPR000276; GPCR Rhodopsin.  
 DR InterPro: IPR000725; Olfact\_receptor.  
 DR Pfam: PF00001; 7tm 1.1.  
 DR PRINTS: PR00237; GPCRHOOPS.  
 DR PRINTS: PR00245; OLFACTORYR.  
 DR PROSITE: PS00237; G-PROTEIN RECP F1\_1; 1.  
 DR PROSITE: PS0262; G-PROTEIN RECP F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 350 AA; 38760 MW; 79D78A979DFD76CC CRC64;  
 Query Match 55.7%; Score 990; DB 2; Length 350;  
 Best Local Similarity 54.8%; Pred. No. 1.5e-66;  
 Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;  
 QY 3 CMPC-----ALPTGGLLHPQHTMMEIANVSSPEVFLGFSARPSLETUFLVILS 54  
 Db 24 CFGCTHSIPALGADPPG-----MGLGNESSLMDFFILLGFSRLEAVLFFVFLF 74  
 QY 55 FYMVSILGNLIIIVSHVTDVHLTPMVFLLANLFLDMSFTTSIVPOLLANLWGPKTIS 114  
 Db 75 FYLLTLVGNFTIIISYLDPLHPMVFLLNLSLLDICTTSIAPQTLNQLRPKXIT 134  
 QY 115 YGGCVQVYISHWLGATECVLLATMSVDYVAACRPLHYTYVMHPQLCLGLALASWLGGL 174  
 Db 135 YGGCVQVYISALGSTECILLADMDALDYIAVCKPLHYVVMNPRLCQQLASISWLSGL 194  
 QY 175 TTSVMGSLTLLPLCGNCCIDHFCFCEMPLIMOLACVDTSINEMEMYLASFVFWVLPLGL 234  
 Db 195 ASSLIHATFTLQLPCLGNRDLHFICEVPALLKLCACVDITVNELVFVSVLFPVIPPAL 254  
 QY 235 ILVSYGHIARAVLKIRSAEGRKAFNFCSSHVAVVSIFYGSIIPMYLOPAKSTSHQCKF 294  
 Db 255 ISISYGFITQAVLRKISVEARHKAFSTCSSHLTVIIFYGTIIIVYLQPSDSVAQOGKF 314  
 QY 295 IALFYVTVPALNPLIYLTANTEVKSALRHMVLENCGSGAKL 337  
 Db 315 ISLFYVTVPALNPLIYLTARNDKMEALRKL-----SGKL 350  
 RESULT 6  
 OL15 MOUSE  
 ID OL15 MOUSE STANDARD; PRT; 312 AA.  
 AC P32275;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Olfactory receptor 15 (OR3).  
 GN Name:Olf15;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP MEDLINE=93028384; PubMed=1384038;  
 RA Nef P., Hermans-Borgmeyer I., Artieres-Pin H., Beasley L.,  
 RA Dionne V.E., Heinemann S.F.;  
 RT "Spatial pattern of receptor expression in the olfactory epithelium.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8948-8952(1992).  
 CC -|- FUNCTION: Putative odorant receptor.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -|- TISSUE SPECIFICITY: Olfactory epithelium.  
 CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 -----

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 EMBL: M84005; AAA39862.1; .  
 FIR; A46247; A46247.  
 MGD; MGI:106182; Olfr15.  
 DR InterPro: IPR000276; GPCR Rhodopsin.  
 DR InterPro: IPR000725; Olfact\_receptor.  
 DR Pfam: PF00001; 7tm 1.1.  
 DR PRINTS: PR00237; GPCRHOOPS.  
 DR PRINTS: PR00245; OLFACTORYR.  
 DR PROSITE: PS00237; G-PROTEIN RECP F1\_1; 1.  
 DR PROSITE: PS0262; G-PROTEIN RECP F1\_2; 1.  
 DR G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;  
 KW Transmembrane.  
 FT DOMAIN 1 24 Extracellular (Potential).  
 FT TRANSMEM 25 48 1 (Potential).  
 FT DOMAIN 49 57 Cytoplasmic (Potential).  
 FT TRANSMEM 58 79 2 (Potential).  
 FT DOMAIN 80 100 Extracellular (Potential).  
 FT TRANSMEM 101 120 3 (Potential).  
 FT DOMAIN 121 139 Cytoplasmic (Potential).  
 FT TRANSMEM 140 160 4 (Potential).  
 FT DOMAIN 161 200 Extracellular (Potential).  
 FT TRANSMEM 201 222 5 (Potential).  
 FT DOMAIN 223 236 Cytoplasmic (Potential).  
 FT TRANSMEM 237 261 6 (Potential).  
 FT DOMAIN 262 272 Extracellular (Potential).  
 FT TRANSMEM 273 292 7 (Potential).  
 FT DOMAIN 293 312 Cytoplasmic (Potential).  
 FT DISULFID 97 189 By similarity.  
 FT CARBOHYD 6 N-linked (GlcNAc..) (Potential).  
 SQ SEQUENCE 312 AA; 34333 MW; 8D3877EBBF5E1E132 CRC64;  
 Query Match 55.5%; Score 985; DB 1; Length 312;  
 Best Local Similarity 60.0%; Pred. No. 3.2e-66;  
 Matches 183; Conservative 50; Mismatches 72; Indels 0; Gaps 0;  
 QY 22 MEIANVSSPEVFLGFSARPSLETUFLVILSVFYMVSILGNLIIIVSHVTDVHLTPMY 81  
 Db 1 MEVDSNSSGTFILMGVSDHPHLEIFFAVILASVLLTILVGNLTILLSLRLDARLTPMY 60  
 QY 82 FFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMSY 141  
 Db 61 FFLSNLSLDAFTTSSVPQMLKNLWGPDKTISYGGCVTQLYVFLWLGATECILLVWMAF 120  
 QY 142 DRYAAICRPLHYTYVMHPQLCLGLALASWLGSLTSMVGSILTMLPLCGNCCIDHPFCE 201  
 Db 121 DRYVAVCRPLHYTYVMNPRLCWGLAASWLGGLGNSVIQSTFTLQLPFCGHRKRVNLFCE 180  
 QY 202 MPLIMQLACVDTSLNEMEMYLASFVFWVLPLGLIIVSYGHIARAVLKIRSAEGRKAFNT 261  
 Db 181 VPAMIKLACGDTSLNEAVLNGVCTFTTVPVSVILVSYCFIAQAQVMKIRSVGRKAFNT 240  
 QY 262 CSHVAVVSYLFGSIIFMYLOPAKSTSHQCKFTALFYVTVPALNPLIYLTARNTVEVKA 321  
 Db 241 CVSHLVVVFYFGSAIYGLLPKSNQSGKFIISFYSVVTPVWVNPVLIYLTARNTVEVKA 300  
 QY 322 LRHMV 326  
 Db 301 LGRLL 305  
 RESULT 7  
 OL23 HUMAN  
 ID OL23 HUMAN STANDARD; PRT; 309 AA.  
 AC Q8NGZ4;  
 DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Olfactory receptor 2G3.  
GN Name=OR2G3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,  
RA Tautumi S., Aburatani H., Asai K., Akiyama Y.;  
RT "Genome-wide discovery and analysis of human seven transmembrane helix  
RT receptor genes.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Putative odorant receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorerium  
CC (HORDE);  
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR ENBL; AB065622; BAC05848.1; -;  
DR Genew; HGNC:15008; OR2G3.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR000725; Olfact\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PRINTS; PR00245; OLFACTORYR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;  
KW Transmembrane.  
FT DOMAIN 1 25 Extracellular (Potential).  
FT TRANSMEM 26 49 1 (Potential).  
FT DOMAIN 50 57 Cytoplasmic (Potential).  
FT TRANSMEM 58 79 2 (Potential).  
FT DOMAIN 80 100 Extracellular (Potential).  
FT TRANSMEM 101 120 3 (Potential).  
FT DOMAIN 121 139 Cytoplasmic (Potential).  
FT TRANSMEM 140 158 4 (Potential).  
FT DOMAIN 159 195 Extracellular (Potential).  
FT TRANSMEM 196 219 5 (Potential).  
FT DOMAIN 220 236 Cytoplasmic (Potential).  
FT TRANSMEM 237 259 6 (Potential).  
FT DOMAIN 260 272 Extracellular (Potential).  
FT TRANSMEM 273 292 7 (Potential).  
FT DOMAIN 293 309 Cytoplasmic (Potential).  
FT DISULFID 97 189 By similarity.  
FT CARBOHYD 5 5 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 309 AA; 34506 MW; F72A80E3A753695C CRC64;  
Query Match 55.4%; Score 984.5; DB 1; Length 309;  
Best Local Similarity 57.6%; Pred. No. 3.5e-66;  
Matches 182; Conservative 63; Mismatches 64; Indels 7; Gaps 1;  
QY 22 MEIANVSPEVFLGFSARSLATVLFIVLVSFVMSILNGIILVSHDTHLTPMY 81  
Db 1 MGLGNESLMDIFLLGSDHRLRAVLVFLFFLLTLVGNFTLIISYLDPLTPMY 60  
QY 82 FFLANLFLDMSFTSTVPQLLANLWGPQKTSYGGCVQVYVISHWLGATECVLLATWSY 141  
Db 61 FFLNLSLLDICFTTSLAPQLVNLQRPKTTITGGCAQVLYISALGSTECLLADWAL 120  
QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMVGSTLTWLLPLCGNCCIDHFFCE 201

Db 121 DRIYVCKPLHYVIVNPRLCQQLASISWLSGLASSLIHATFTLQLPLCGNHRLDHFICE 180  
QY 202 MPLIMQLACVDTSLNEMMYLASFVVFVPLGLILVSYGHARAVLAKIRSAEGRKAFNT 261  
Db 181 VPALLKLACVDTTWNELVFWVSVLFWIPALISISYGFITQAVLRKISVEARHKAFST 240  
QY 262 CSSHVAVVSLFYGSIIIPMYLOPAKSTSHQKFTALEYTVTPALNPLIYTLRNTVKSA 321  
Db 241 CSSHLTVIIFYGTIIYVYVLPQSDSYAQDQKFTLSLFTYTWPTPLNPIYTLRNMKEA 300  
QY 322 LRHMVLENCGSGAKL 337  
Db 301 LRKLL-----SGKL 309  
RESULT 8  
ID Q8VFF0 PRELIMINARY; PRT; 312 AA.  
AC Q8VFF0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Olfactory receptor MOR256-17 (Olfactory receptor Olfr15).  
GN Name=Olfr15; (Mouse).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21676863; PubMed=11802173;  
RA Zhang X., Firestein S.;  
RT "The olfactory receptor gene superfamily of the mouse.";  
RL Nat. Neurosci. 5:124-133(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;  
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,  
RA Trask B.J.;  
RT "Different evolutionary processes shaped the mouse and human olfactory  
RT receptor gene families.";  
RL Hum. Mol. Genet. 11:535-546(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Adams M.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;  
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,  
RA Walker M., Williams E.M., Trask B.J.;  
RT "Odorant receptor expressed sequence tags demonstrate olfactory  
RT expression of over 400 genes, extensive alternate splicing and unequal  
RT expression levels.";  
RL Genome Biol. 4:R71-R71(2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Sanders K.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AY073576; AAL61239.1; -;  
DR EMBL; AY317256; AAP70766.1; -;  
DR MGD; MGI:106182; Olfr15.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PRINTS; PR00245; OLFACTORYR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 312 AA; 34319 MW; DC7E30EBBD0750E9 CRC64;







DR EMBL; AJ302554; CAC21442.1; -  
 DR EMBL; AJ302555; CAC21443.1; -  
 DR EMBL; AJ302556; CAC21444.1; -  
 DR EMBL; AJ302557; CAC20477.1; -  
 DR EMBL; AJ302558; CAC20478.1; -  
 DR EMBL; AF399630; AAK95115.1; -  
 DR Genew; HGNC:8261; OR2J3.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR000725; Olfact\_receptor.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PRINTS; PR00245; OLFACTORYR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 DR G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;  
 KW Polymorphism; Transmembrane.  
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 FT DOMAIN 53 60 Cytoplasmic (Potential).  
 FT TRANSMEM 61 82 2 (Potential).  
 FT DOMAIN 83 103 Extracellular (Potential).  
 FT TRANSMEM 104 123 3 (Potential).  
 FT DOMAIN 124 142 Cytoplasmic (Potential).  
 FT TRANSMEM 143 161 4 (Potential).  
 FT DOMAIN 162 198 Extracellular (Potential).  
 FT TRANSMEM 199 222 5 (Potential).  
 FT DOMAIN 223 239 Cytoplasmic (Potential).  
 FT TRANSMEM 240 262 6 (Potential).  
 FT DOMAIN 263 275 Extracellular (Potential).  
 FT TRANSMEM 276 295 7 (Potential).  
 FT DOMAIN 296 311 Cytoplasmic (Potential).  
 FT DISULFID 100 192 By similarity.  
 FT CARBOHYD 8 8 N-linked (GlcNAc. .) (Potential).  
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 FT VARIANT 226 226 R -> Q (in allele 6M1-3\*02).  
 FT VARIANT 228 228 V -> I (in allele 6M1-3\*03).  
 FT VARIANT 261 261 /FTID=VAR\_010950.  
 FT VARIANT 261 261 /FTID=VAR\_010951.  
 FT VARIANT 261 261 I -> M (in allele 6M1-3\*03 and allele 6M1-3\*04).  
 FT SEQUENCE 311 AA; 34950 MW; 84201145B9D5AA68 CRC64;  
 Query Match 54.7%; Score 972; DB 1; Length 311;  
 Best Local Similarity 58.1%; Pred. No. 3.1e-65;  
 Matches 175; Conservative 57; Mismatches 69; Indels 0; Gaps 0;  
 QY 26 NVSSPEFVLLGFSARPSLETVLFIIVLVSFYMWISLNGIILVSHVDVHLHTPMYFLA 85  
 DB 8 NASSEGYFIILVGFNSWPHLEVIIVVVLIFYLMTLIGNLIILSYLDSHLHTPMYFLS 67  
 QY 86 NLSPFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVQFVISHWLGCATECVLLATMSYD 145  
 DB 68 NLSPFLDLCYTTSIPOLLVNLWGPKTISYAGCMQILYFVALGTTCVLLVMSYD 127  
 QY 146 AICRPLHYTVMHPQLCLGLALASWLGLTTSVMVSGTTLTMLPLCGNCCIDHFFCEMPLI 205  
 DB 128 AVCRPLHYTVMHPFCHLLAVASWVSGFTNSALHSSFTFWPLCGHQVDHFFCEVPAL 187  
 QY 206 MQLACVDTSLNEMEMYLASFVFWVLPLGLILVSYGHIAVAVLKIRSGRRKAPNTCSSH 265  
 DB 188 LRLSCVDTHVNELTMTTISFVLIPILILTSYGAIKIRSVAVLRMQSTGLQKVFCTGAH 247  
 QY 266 VAVVSLFYSGSIIFMYLQPAKSTSHQCKFIATFYVTVTPALNPLIYTLRNTVEKSA 325  
 DB 248 LMAVSLFFIPAMCIYLPQPSGNSQDQKFIATFYVTVTPSLNPLIYTLRNVKVRGAVKRL 307  
 QY 326 V 326  
 DB 308 M 308

RESULT 14  
 ID Q7TQ02 PRELIMINARY; PRT; 308 AA.  
 AC Q7TQ02;  
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Olfactory receptor Olfr1362.  
 GN NamesOlfr1362;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;  
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,  
 RA Walker M., Williams E.M., Traak B.J.;  
 RT "Odorant receptor expressed sequence tags demonstrate olfactory  
 RT expression of over 400 genes, extensive alternate splicing and unequal  
 RT expression levels.";  
 RL Genome Biol. 4:R71-R71 (2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sanders K.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY318572; AAP71747.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 308 AA; 34477 MW; 5426728184F16EEF CRC64;  
 Query Match 54.7%; Score 971.5; DB 2; Length 308;  
 Best Local Similarity 60.5%; Pred. No. 3.3e-65;  
 Matches 188; Conservative 43; Mismatches 75; Indels 5; Gaps 1;  
 QY 22 METANVSSPEFVLLGFSARPSLETVLFIIVLVSFYMWISLNGIILVSHVDVHLHTPMY 81  
 DB 1 MEKNSDSSEYGFLEGFSRPLEWLVFIYNFLYSVAVLGNITILVCLDPLRLHTPMY 60  
 QY 82 FFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVQFVISHWLGCATECVLLATMSY 141  
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 QY 322 LRHMVLENC CG 332  
 DB 301 LKKV-----CG 306

RESULT 15  
 ID O2B8 HUMAN  
 AC P59922;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2005, 17:03:09 ; Search time 43 Seconds  
(without alignments)  
590.248 Million cell updates/sec

Title: US-10-633-894-6

Perfect score: 1776

Sequence: 1 MPCMPALPTGGLPHQHT.....ALRHMVLECCSAGKLAQI 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1776	100.0	340	4	US-09-546-986A-6
2	1776	100.0	340	4	US-09-524-730-6
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4	977	55.0	334	4	US-09-524-730-8
5	902	50.8	310	4	US-09-546-986A-2
6	902	50.8	310	4	US-09-524-730-2
7	823	46.3	331	4	US-09-546-986A-4
8	823	46.3	331	4	US-09-524-730-4
9	703	39.6	309	3	US-08-988-876-5
10	674	38.0	316	2	US-08-827-291A-2
11	672	37.8	314	3	US-08-988-876-7
12	672	37.8	314	4	US-09-968-033C-5
13	671.5	37.8	313	4	US-09-465-901-48
14	669	37.7	321	3	US-08-748-506-10
15	668	37.6	321	3	US-08-748-506-19
16	667	37.6	321	3	US-08-748-506-11
17	667	37.6	321	3	US-08-748-506-18
18	653	36.8	321	3	US-08-748-506-12
19	651	36.7	321	3	US-08-748-506-20
20	648	36.5	321	3	US-08-748-506-13
21	637.5	35.9	296	2	US-08-467-948A-2
22	637.5	35.9	296	3	US-08-467-947A-2
23	634	35.7	333	3	US-08-988-876-6
24	609	34.3	284	1	US-08-118-270-61
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27	596	33.6	277	5	PCT-US93-08528-62

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Sequence 14, Appl  
Sequence 24, Appl  
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Sequence 65, Appl  
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28 576.5 32.5 284 1 US-08-118-270-67  
29 576.5 32.5 284 5 PCT-US93-08528-67  
30 564 31.8 247 1 US-08-465-980-3  
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32 564 31.8 247 3 US-09-339-115-3  
33 564 31.8 247 5 PCT-US95-07093-3  
34 561.5 31.6 274 1 US-08-118-270-69  
35 561.5 31.6 274 5 PCT-US93-08528-69  
36 555.5 31.3 269 1 US-08-118-270-64  
37 555.5 31.3 269 5 PCT-US93-08528-64  
38 543 30.6 327 3 US-08-748-506-14  
39 540 30.4 327 3 US-08-748-506-24  
40 537.5 30.3 293 1 US-08-118-270-60  
41 537.5 30.3 293 5 PCT-US93-08528-60  
42 537 30.2 327 3 US-08-748-506-22  
43 537 30.2 327 3 US-08-748-506-23  
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45 535.5 30.2 286 5 PCT-US93-08528-65

## ALIGNMENTS

RESULT 1  
US-09-546-986A-6  
; Sequence 6, Application US/09546986A  
; Patent No. 6635741  
; GENERAL INFORMATION:  
; APPLICANT: Powers, Scott  
; APPLICANT: Yang, Jianxin  
; APPLICANT: Cutler, Gene  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors  
; FILE REFERENCE: 018781-004720US  
; CURRENT APPLICATION NUMBER: US/09/546.986A  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 09/524,730  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; ORGANISM: US-09-546-986A-6

Query Match 100.0%; Score 1776; DB 4; Length 340;  
Best Local Similarity 100.0%; Pred. No. 7.9e-149;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPCMPALPTGGLPHQHTMMEIANVSSPEVFLGFSARPSETLVLFIVLVSFYMWSI 60  
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Qy 121 QFYIHWLGATECVLLATMSYDRAAICRPLHVTVMHPOLCLGLALASWLGGLTTSV 180  
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Db 181 STLTMLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFPVPLGLILV 240

Qy 241 HIARAVLKIRSAGRKKAFTNCSSHVAVWSLFGSIIIFMYLOPAKSTSHGCKFIAL 300  
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Qy 301 VVTPALNPLIYTYRNTTEVKSALRHMVLECCSAGKLAQI 340  
Db 301 VVTPALNPLIYTYRNTTEVKSALRHMVLECCSAGKLAQI 340

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RESULT 2
US-09-524-730-6
; Sequence 6, Application US/09524730
; Patent No. 6638733
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004710US
; CURRENT APPLICATION NUMBER: US/09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-524-730-6

Query Match      100.0%; Score 1776; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 7.9e-149; Indels 0; Gaps 0;
Matches 340; Conservative 0; Mismatches 0;

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QY 61 LGNGIILVSTVDHLHPTMPYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVV 120
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QY 121 QFYLSHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVG 180
DB 121 QFYLSHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVG 180

QY 181 STLTMPLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFPVPLPLGLILVSYG 240
DB 181 STLTMPLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFPVPLPLGLILVSYG 240

QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSILFYGSIIFMYLOPAKSTSHQGFIALFYT 300
DB 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSILFYGSIIFMYLOPAKSTSHQGFIALFYT 300

QY 301 VVTPALNPLIYTLRNTVEKSGALRHVLENCGSGAGKLAQI 340
DB 301 VVTPALNPLIYTLRNTVEKSGALRHVLENCGSGAGKLAQI 340

RESULT 3
US-09-546-986A-8
; Sequence 8, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-546-986A-8

Query Match      55.0%; Score 977; DB 4; Length 334;
Best Local Similarity 58.5%; Pred. No. 2.3e-78; Indels 4; Gaps 1;
Matches 183; Conservative 58; Mismatches 68;

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QY 74 VHLHPTMPYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVVQFYISHWLGATEC 133
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QY 134 VLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTLTMLPLCGNN 193
DB 133 VLPALMSCDRYAVCRPLHYTVIMHILCMALASWANLSGIATTLVQSTLTTLQLPFCGHR 192

QY 194 CIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFPVPLPLGLIILVSYGHIAVLRKIRSAE 253
DB 193 QVDHFICEVPVLKICACVGTTFNEAELEFVASILFLIVPVSVFILVSSGYIAHAVLRKISAT 252

QY 254 GRRKAFNTCSSHVAVVSILFYGSIIFMYLOPAKSTSHQGFIALFYTVVTPALNPLIYTL 313
DB 253 GROKAFGTCTSHLTVTVTIIFYGTIIFMYLOPAKSRSDQGFVSLFYTVVTVVTRMLNPLIYTL 312

QY 314 RNTEVKSALRHMV 326
DB 313 RIKEVKGALKVIL 325

RESULT 4
US-09-524-730-8
; Sequence 8, Application US/09524730
; Patent No. 6638733
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004710US
; CURRENT APPLICATION NUMBER: US/09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-524-730-8

Query Match      55.0%; Score 977; DB 4; Length 334;
Best Local Similarity 58.5%; Pred. No. 2.3e-78; Indels 4; Gaps 1;
Matches 183; Conservative 58; Mismatches 68;

QY 18 QHT----MMEIANVSSPEVFLVLLGFSARPSETLVFIVLSFYMVSIILGNGIILVSHSTD 73
DB 13 EHTLHGMVVRHTNESNLGAGFILLGFSQDYAQLQKLVFLVILLYLTILGNTTILVSRLE 72

QY 74 VHLHPTMPYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVVQFYISHWLGATEC 133
DB 73 PKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLNLSHALGSTEC 132

QY 134 VLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTLTMLPLCGNN 193
DB 133 VLPALMSCDRYAVCRPLHYTVIMHILCMALASWANLSGIATTLVQSTLTTLQLPFCGHR 192

QY 194 CIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFPVPLPLGLIILVSYGHIAVLRKIRSAE 253
DB 193 QVDHFICEVPVLKICACVGTTFNEAELEFVASILFLIVPVSVFILVSSGYIAHAVLRKISAT 252

QY 254 GRRKAFNTCSSHVAVVSILFYGSIIFMYLOPAKSTSHQGFIALFYTVVTPALNPLIYTL 313
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Db      253 GRQKAFGTCFFSHLTVTWTFYGTITPMYLPQAKSRDQCKFVSLFYVTWTRMLNPLIYTL 312
Qy      314 RNTVEVKSALRHMV 326
Db      313 RIKEVKGALKKVL 325

RESULT 5
US-09-546-986A-2
; Sequence 2, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 2
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-986A-2

Query Match      50.8%; Score 902; DB 4; Length 310;
Best Local Similarity 54.2%; Pred. No. 8.8e-72;
Matches 166; Conservative 57; Mismatches 81; Indels 2; Gaps 1

Qy      29 SPEVFVLGFSARPSLETVLFIIVLSFWMVSLNGIIILVSHTDVHLHTPMYFPLANLS 88
Db      5 SPKAFILIGVSDRPWLELPFLFVLLLSVLAAMLGNVAIILASRVDPLQFHSPMYIFLSHLS 64
Qy      89 FLDSMFTTSIYPLLANIWGPKQTSYGGCVVQFYISHWLGATECVLLATMSYDHYAIC 148
Db      65 FLDCYCTITVTTPQMLVNMGSSQKTSYGGCTVQYAVFHWLGTCTCIVLAAMDRIYVASC 124
Qy      149 RPLHYVTIMHPQLCLGLALASWLGGLTTSVMVGSTLTMLPLCGNCCIDHFFCEMFLIMQL 208
Db      125 KPLHYAVLMHRALCQQLVALAWLSGFGNSFVQVVLTVQLPFCGRQVLNFFCEVPAVIK 184
Qy      209 ACVDTSLNEMEWYLASFVFVVLPLGLIILVSGHIAARVLKTRASGRKAKFNTCSSHVAV 268
Db      185 SCADTAMNDTTLAVLAVFVLVPLAILLSYGFIAARVLIQSSGRHKAFCGTCSSHLMI 244
Qy      269 VSLFVGSITFMVLPQAKSTSEOGKFALFYVTWTPALNPLIYTLNTEVKSALRHMV-- 326
Db      245 VSLFVLPALMYLOPPSSYQEQGKFISLFSYIITPTLNPFTYTLRNKMDKMGALRRLLAR 304
Qy      327 LENCQG 332
Db      305 IWRLCG 310

RESULT 6
US-09-524-730-2
; Sequence 2, Application US/09524730
; Patent No. 6638733
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004710US
; CURRENT APPLICATION NUMBER: US/09/524,730
; CURRENT FILING DATE: 2000-03-14

```

Db 125 AVCRSLHYMAVRPHLCQLQVTVVAVCCGFLNSFIMCPQWQLSRCRRRVDHFLCEMPAL 184  
Qy 206 MQLACVDTSLNEMEMYLASFVFLV-----PLGLILVS---YGHIAVAVLKIRSAEGR 256  
Db 185 IAMSCEETMLVEA-----IHLCPGGSPGGAALPHPHLYGVIAAALVRMKSAAGRK 235  
Qy 257 KAFNTCSSHVVAVSLFYGSIIFMYLQPAKSTHEQGFALFYVTVTPALNPLIYTLRNT 316  
Db 236 KAFHTCSSLTVVSLFYGTIIIVYLKPAANSYSDQGRFLTYFTIVIPSNPLIYTLRNK 295  
Qy 317 EVKSALRHMV 326  
Db 296 DVKGTWKLL 305

## RESULT 8

US-09-524-730-4  
; Sequence 4, Application US/09524730  
; Patent No. 6638733  
; GENERAL INFORMATION:  
; APPLICANT: Powers, Scott  
; APPLICANT: Yang, Jianxin  
; APPLICANT: Cutler, Gene  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors  
; FILE REFERENCE: 018781-004710US  
; CURRENT APPLICATION NUMBER: US/09/524,730  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-524-730-4

Query Match 46.3%; Score 823; DB 4; Length 331;  
Best Local Similarity 52.3%; Pred. No. 8.8e-65;  
Matches 162; Conservative 47; Mismatches 83; Indels 18; Gaps 3;  
Qy 26 NVSPPEVVLGFSARPSLETVLFIIVLSFVMSILGNGIILVSHSTDVHLHTPMYFFLA 85  
Db 5 NASYLOAPILVGGSDRPGLEKILFAVILFCILTVGNTAILLLVMDVRLHTPMYFFLG 64  
Qy 86 NLSFLDMSFTTSIVPQLLANLWGPKTISYGGCVQYVISHWLGATECVLLATMSVDRYA 145  
Db 65 NLSFLDLCFTASIAPOALLMNLGGPEKITYHGCVAQLIYIMMLGSTECVLLVWMSHDYV 124  
Qy 146 AICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSLTLLPLCGNCCIDHFCWPLI 205  
Db 125 AVCRSLHYMAVRPHLCQLQVTVVAVCCGFLNSFIMCPQWQLSRCRRRVDHFLCEMPAL 184  
Qy 206 MQLACVDTSLNEMEMYLASFVFLV-----PLGLILVS---YGHIAVAVLKIRSAEGR 256  
Db 185 IAMSCEETMLVEA-----IHLCPGGSPGGAALPHPHLYGVIAAALVRMKSAAGRK 235  
Qy 257 KAFNTCSSHVVAVSLFYGSIIFMYLQPAKSTHEQGFALFYVTVTPALNPLIYTLRNT 316  
Db 236 KAFHTCSSLTVVSLFYGTIIIVYLKPAANSYSDQGRFLTYFTIVIPSNPLIYTLRNK 295  
Qy 317 EVKSALRHMV 326  
Db 296 DVKGTWKLL 305

## RESULT 9

US-08-988-876-5  
; Sequence 5, Application US/08988876  
; Patent No. 6063596  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/988,876  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0441 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 309 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1314667  
; US-08-988-876-5

Query Match 39.6%; Score 703; DB 3; Length 309;  
Best Local Similarity 46.5%; Pred. No. 3.1e-54;  
Matches 140; Conservative 53; Mismatches 108; Indels 0; Gaps 0;

Qy 22 MEIANVSPPEVVLGFSARPSLETVLFIIVLSFVMSILGNGIILVSHSTDVHLHTPMY 81  
Db 1 MELENDTRIPBFLLLGFSPEEPKLPFLGFLSMYLVLTILGNLLILAVSSDHLTPMY 60  
Qy 82 FFANLSFLDMSFTTSIVPQLLANLWGPKTISYGGCVQYVISHWLGATECVLLATMSY 141  
Db 61 FFANLSFVDICFTCTTIPKMLVNIQTKVITVESCIIQMYFELFAGIDNFLTUNWAY 120  
Qy 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSLTLLPLCGNCCIDHFFCE 201  
Db 121 DRYMAICYPLHYMVMNPQLCGLSLLLVSWIMSALSLIQLTMLVRLSFTCTHFPHPFCE 180  
Qy 202 MPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSVGHIAVAVLKIRSAEGRKAFNT 261  
Db 181 LNMQLACSDTFLNNMMLYFAAILLVGAPLVGLVSYFKIVSVSSIRGISSAHSKYKAFST 240  
Qy 262 CSHVAVVSLFYGSIIFMYLQPAKSTHEQGFALFYVTVTPALNPLIYTLRNTVKSA 321  
Db 241 CASHLSVSVSLFYCTSLGVYLSSAAPQSTHTSSVASVAVMYTVVTPMLNPNFIYSLRNKDIGA 300  
Qy 322 L 322  
Db 301 L 301

RESULT 10

US-08-827-291A-2  
; Sequence 2, Application US/08827291A  
; Patent No. 5874243  
; GENERAL INFORMATION:  
; APPLICANT: Macina, Roberto  
; APPLICANT: Sathé, Ganesh  
; TITLE OF INVENTION: NOVEL OLRCC15 RECEPTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/827,291A  
; FILING DATE: 28-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: GP50001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5015  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 316 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-827-291A-2

Query Match 38.0%; Score 674; DB 2; Length 316;  
Best Local Similarity 43.3%; Pred. No. 1.2e-51;  
Matches 125; Conservative 56; Mismatches 108; Indels 0; Gaps 0;  
Qy 33 FVLLGFSARPSLETVFIIVLSFYMWVSIILNGIIIVSHVTDVHLHTPMYFFLANLSPLDM 92  
Db 12 FIFLGIFNHSPTHTFLFLVLAIFSVAFMGNSVMVLLIYDQTQHTPMYLLLSQLSIMDL 71  
Qy 93 SFTTSIVPOLANLWGPQKTSYGGCVQFYISHWLGATECVLLATMSYDRAAICRPLH 152  
Db 72 MLCITVPKAFNYLGSKSIWAGCATQIFFTYLLGSECFLLAVWAYDYTAICHPLR 131  
Qy 153 YTVIMHPQLCLGALASWLGGLTTSVMGSLTLMPLCGNCCIDHFFCEMPLIMQLACVD 212  
Db 132 YTNLMPKICGLTAFSWILGSDGIIYAVATFSYCGSREIAHPPELPSLLILSCND 191  
Qy 213 TSLNEMMYLASFVFFVPLGLILVSGHITARAVALKIRSAEGRKAFNTCSSHVAVSLF 272  
Db 192 TSIFKEVIFTCISVLMVFPVAIIIASYAGVILAVIHMGSGEGRKAFNTCSSHLVVGMP 251  
Qy 273 YGSIIFWLPQAKSTSEHQKGFIALFVTVTPALNPLIYTLRNTVEKSA 321  
Db 252 YGAGLFMYIQTSRDSPTQDKLVSVFTIITPLMLNPLIYSLRNKEVTRA 300

## RESULT 11

US-08-988-876-7  
; Sequence 7, Application US/08988876  
; Patent No. 6063596

; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/988,876  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0441 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 32086  
US-08-988-876-7  
Query Match 37.8%; Score 672; DB 3; Length 314;  
Best Local Similarity 43.9%; Pred. No. 1.7e-51;  
Matches 133; Conservative 62; Mismatches 104; Indels 4; Gaps 2;  
Qy 26 NVSSPEVFLGFSARPSLETVFIIVLSFYMWVSIILNGIIIVSHVTDVHLHTPMYFFLA 85  
Db 5 NQTSISDFLLGLPIQEQONLCYALFLAMYLTLGLNLLIIVLRDLSHLHTPMYFLS 64  
Qy 86 NLSFLDMSFTTSIVPOLANLWGPQKTSYGGCVQFYISHWLGATECVLLATMSYDRA 145  
Db 65 NLSFSLCSESVTIPKLLQNMQNDPSIPYADCLTQMYFLLFGDLESFLLVAMAYDRYV 124  
Qy 146 AICRPLHYTVIMHPQLCLGALASWLGGLTTSVMGSLTLMPLCGNCCIDHFFCEMP 203  
Db 125 AICFPLHYTAIMSPMLCLALVALSWV--LTFHAMLHTLLMARLCFCADNVIPHFFCDMS 182  
Qy 204 LIMQLACVDTSLNEMMYLASFVFFVPLGLILVSGHITARAVALKIRSAEGRKAFNTCS 263  
Db 183 ALLKLAFSDTRVNEWVIFMGGLILVIFLFLILGSYARIVSSILKVPSSKIGICKAFSTCG 242  
Qy 264 SHVAVSLFVGSIIFMVLPQAKSTSEHQKGFIALFVTVTPALNPLIYTLRNTVEKSA 323  
Db 243 SHLSVSVSLFYGTIGVLYLCSSANSTLKQTVAMMYTVTVTPMLNPFYISLRNRMKGALS 302  
Qy 324 HMV 326  
Db 303 RVI 305



LENGTH: 321 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-748-506-10

Query Match 37.7%; Score 669; DB 3; Length 321;

Best Local Similarity 47.1%; Pred. No. 3.3e-51; Mismatches 108; Indels 0; Gaps 0;

Matches 137; Conservative 46; Mismatches 108; Indels 0; Gaps 0;

Qy 33 FVLGFSARPSLETVLFIIVLVSFVMSILGNGIILVSHDTHLHTPMYFFLANLSFLDM 92  
Db 18 FAFKFSVEVGECEFLFNLLMLVSLTGNLIVLAICTSPSLHTPMYFFLANLSLEI 77

Qy 93 SFTTSIVPQLLANIWMGPKQTSISYGGCVVQFYISHWLGAETCVLLATWSYDYRYAAICRPLH 152  
Db 78 GYTCSVIPKMLQSLVSEAREISREGCATOMFFPAFFGITECCLLAAMAFDRCMAICSPHL 137

Qy 153 YTVIMHPQLCLGLALASWLGGLTTSVMVGSSTLTMLPLCGNNCIDHFFCEMPLIMQLACVD 212  
Db 138 YATRMSREVCAHLAIVSWGMCIVSLGQTNFIFSLNFCGPEIDHFFCDLPPLLALACGD 197

Qy 213 TSLNEMEMYLASFVVFVVLPLGLILVSYGHIAARAVLKIRSAEGRKAFNTCSSHVAVVSLF 272  
Db 198 TSQNEAIFVAVVLCISSPFLIIYSVKILIAVLLMPSPEGRHKALSTCSSHLLVVTLF 257

Qy 273 YGSIIFMYLOPAKSTSHQKQKFTALFYVTVTPALNPLIYTLRNTVEVKSALR 323  
Db 258 YGSACITYLRPKSSHSPGMDKFLALFYVTVTSMNLNPIIYSLRNKEVKAALR 308

RESULT 15

US-08-748-506-19  
Sequence 19, Application US/08748506  
Patent No. 6159707  
GENERAL INFORMATION:  
APPLICANT: Ronnett et al.  
TITLE OF INVENTION: NOVEL SPERM RECEPTORS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: IL  
COUNTRY: US  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,506  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,751  
FILING DATE: 09-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 74940  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5600  
TELEFAX: 312-616-5700  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-748-506-19

Query Match 37.6%; Score 668; DB 3; Length 321;

Best Local Similarity 46.0%; Pred. No. 4e-51; Mismatches 112; Indels 0; Gaps 0;

Matches 137; Conservative 49; Mismatches 112; Indels 0; Gaps 0;

Qy 26 NVSPSEVFLVLLGFSARPSLETVLFIIVLVSFVMSILGNGIILVSHDTHLHTPMYFFLA 85  
Db 11 NSLSVKRFAPAKFSVEVGECEFLFNLLMLVSLTGNALIALAACTSPSLHTPMYFFLA 70

Qy 86 NLSFLDMSFTTSIVPQLLANIWMGPKQTSISYGGCVVQFYISHWLGAETCVLLATWSYDYRYA 145  
Db 71 NLSLEIGYTCVPIPKMLQSLVSEAREISREGCATOMFFFTFFGITECCLLAAMAFDRCM 130

Qy 146 AICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMVGSSTLTMLPLCGNNCIDHFFCEMPLI 205  
Db 131 GICSPHYATRMSREVCAHLAIVSWGMCIVGLGQTNIIISLNFSGPCEIDHFFCDLPP 190

Qy 206 MQLACVDTSLNEMEMYLASFVVFVVLPLGLILVSYGHIAARAVLKIRSAEGRKAFNTCSSH 265  
Db 191 LALACGDTSQNEAIFVAAITLCISSPFLVILYSVIRILVAVLVMPSPGRHKALSTCSSH 250

Qy 266 VAVVSLFYGSIIFMYLOPAKSTSHQKQKFTALFYVTVTPALNPLIYTLRNTVEVKSALR 323  
Db 251 LLVVTLFYGSVSTYLRPKSSHSPGMDKLLALFYVTVTSMNLNPIIYSLRNKEVKAALR 308

Search completed: April 8, 2005, 17:13:16

Job time : 45 secs



GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: April 8, 2005, 16:53:23 ; Search time 173 Seconds  
(without alignments)  
760.107 Million cell updates/sec

Title: US-10-633-894-6  
Perfect score: 1776  
Sequence: 1 MPCMPALPGGLLPHPQHT.....ALRHVLENCSSAGKLAQI 340

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1776	100.0	340	4	AAG67467 Breast am
2	1776	100.0	340	6	ABR63705 Human G-p
3	1767	99.5	340	4	AAU24748 Human olf
4	1767	99.5	340	5	AAU85368 G-coupled
5	1755	98.8	337	6	ABR63707 Human G-p
6	1725	97.1	377	5	ABP95893 Human GPC
7	1654	93.1	320	5	ABR63708 Human G-p
8	1651	93.0	320	5	ABG66931 Novel G-p
9	1649	92.8	319	6	ABR63709 Human G-p
10	1646	92.7	320	5	ABJ04731 GPCR 11 p
11	1645	92.6	320	7	ADC86041 Human GPC
12	1641	92.4	319	4	AAG71912 Human olf
13	1641	92.4	319	4	AAG71896 Human olf
14	1640	92.3	319	6	ABU11186 Human G-p
15	1617	91.0	314	5	ABG76850 Human G-p
16	1565	88.1	305	5	ABJ04026 Human G-p
17	1565	88.1	305	8	ADH30926 Human G-p
18	990	55.7	350	4	AAU24714 Human olf
19	990	55.7	350	5	ABP95880 Human GPC
20	990	55.7	350	5	AAU85334 G-coupled
21	989	55.7	315	5	AAE18279 Human G-p
22	985	55.5	312	4	AAG72908 Human olf
23	985	55.5	312	4	AAG73035 Olfactory
24	985	55.5	312	8	ADH42027 Novel hum
25	985	55.5	334	5	ABB81444 Human GPC

26	984.5	55.4	309	4	AAG71891	Aag71891 Human olf
27	984.5	55.4	309	5	AAB71353	Aab71353 Human GCR
28	984.5	55.4	309	5	AAE18266	Aae18266 Human G-p
29	984.5	55.4	309	5	AAU95676	Aau95676 Human olf
30	984.5	55.4	309	5	ABB81445	Abb81445 Human GPC
31	984.5	55.4	309	7	ADC85565	Adc85565 Human GPC
32	984.5	55.4	309	7	ADJ83120	Adj83120 Human pro
33	984.5	55.4	314	6	ABR01597	Abr01597 Human G p
34	984	55.4	312	4	AAE10685	Aae10685 G-protein
35	984	55.4	312	8	ADH42039	Adh42039 Novel hum
36	984	55.4	312	8	ADH42041	Adh42041 Novel hum
37	984	55.4	334	4	AAU24698	Aau24698 Human olf
38	984	55.4	334	5	AAU85318	Aau85318 G-coupled
39	982	55.3	315	5	AAE18276	Aae18276 Human G-p
40	981	55.2	315	5	AAE18268	Aae18268 Human G-p
41	981	55.2	315	5	AAE18277	Aae18277 Human G-p
42	980	55.2	334	4	AAG72062	Aag72062 Human olf
43	979	55.1	311	8	ADH42037	Adh42037 Novel hum
44	979	55.1	311	8	ADH42047	Adh42047 Novel hum
45	979	55.1	315	5	AAE18275	Aae18275 Human G-p

ALIGNMENTS

RESULT 1  
AAG67467  
ID AAG67467 standard; protein; 340 AA.  
XX

AC AAG67467;

XX 26-NOV-2001 (first entry)

DE DE Breast amplified G protein coupled receptor (BCA-GPCR)-3.

XX KW Breast amplified G protein coupled receptor; BCA-GPCR; breast cancer;  
chromosome 1q44; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3; BCA-GPCR-4;  
signal transduction.

XX OS Homo sapiens.

XX PN WC200168704-A2.

XX PD 20-SEP-2001.

XX PF 13-MAR-2001; 2001WO-US008020.

XX PR 14-MAR-2000; 2000US-00524730.

XX PR 11-APR-2000; 2000US-00546986.

XX (TULA-) TULARIK INC.

PA (POWE/) POWERS S.

PA (YANG/) YANG J.

PA (CUTL/) CUTLER G.

XX Powers S, Yang J, Cutler G;

PT WPI; 2001-570865/64.

XX N-PSDB; AAH78085.

PT Four nucleic acids encoding breast amplified G protein coupled receptors  
(BCA-GPCRs), useful for identifying modulators of G-protein coupled  
receptor signal transduction which can be used in the treatment of cancer  
such as breast cancer.

XX Claim 14; Page 67-68; 68pp; English.

CC The present sequence represents breast amplified G protein coupled  
receptor (BCA-GPCR)-3. BCA-GPCRs are amplified and/or overexpressed in  
breast cancer cells. The BCA-GPCRs are located at chromosome 1q44, in the  
following orientation (starting from the centromere end): BCA-GPCR-1 (3'-  
5' orientation), BCA-GPCR-2 (5'-3' orientation), BCA-GPCR-3 (3'-5'  
orientation), and BCA-GPCR-4 (5'-3' orientation). The G protein coupled

CC receptors are useful for assaying and identifying modulators of G-protein  
 CC coupled receptor signal transduction. The modulators and antibodies  
 CC against the G protein coupled receptors are useful for pharmacological  
 CC modulation of signalling pathways, e.g. in cancer cells such as breast  
 CC cancer  
 XX  
 SQ Sequence 340 AA;

Query Match 100.0%; Score 1776; DB 4; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-187;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSI 60  
 DB 1 MPCPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSI 60

QY 61 LGNGIILVSHDTHLHTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVV 120  
 DB 61 LGNGIILVSHDTHLHTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVV 120

QY 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVG 180  
 DB 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVG 180

QY 181 STLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
 DB 181 STLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240

QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIIPMYLQPAKSTSHQKFIALFYT 300  
 DB 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIIPMYLQPAKSTSHQKFIALFYT 300

QY 301 VVTPALNPLIYTLRNTVEKSAHRHMVLENCSSAGKLAQI 340  
 DB 301 VVTPALNPLIYTLRNTVEKSAHRHMVLENCSSAGKLAQI 340

## RESULT 2

ABR63705  
 ID ABR63705 standard; protein; 340 AA.  
 XX  
 AC ABR63705;  
 XX  
 DT 29-SEP-2003 (first entry)  
 XX  
 DE Human G-protein coupled receptor BCA-GPCR-3.  
 XX  
 KW Human; G-protein coupled receptor; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3;  
 KW BCA-GPCR-4; breast cancer; cytostatic; cancer; prostate cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003054542-A1.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 18-DEC-2002; 2002WO-US041112.  
 XX  
 PR 20-DEC-2001; 2001US-00028521.  
 XX  
 PA (TULA-) TULARIK INC.  
 XX  
 PI Powers S, Yang J, Cutler G;  
 XX  
 DR WPI; 2003-569288/53.  
 DR N-PSDB; ACC85511.  
 XX  
 PT New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,  
 PT useful for treating cancer, e.g. breast or prostate cancer.  
 XX  
 EX Example 1; Page 62-63; 77pp; English.

The present invention provides the protein and coding sequences of four

CC novel human G-protein coupled receptors (GPCR) which are amplified in  
 CC breast cancers. The sequences are useful in the treatment of cancers,  
 CC including breast and prostate cancers. The present sequence is a GPCR of  
 CC the invention  
 XX  
 SQ Sequence 340 AA;

Query Match 100.0%; Score 1776; DB 6; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-187;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSI 60  
 DB 1 MPCPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSI 60

QY 61 LGNGIILVSHDTHLHTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVV 120  
 DB 61 LGNGIILVSHDTHLHTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVV 120

QY 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVG 180  
 DB 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVG 180

QY 181 STLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
 DB 181 STLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240

QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIIPMYLQPAKSTSHQKFIALFYT 300  
 DB 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIIPMYLQPAKSTSHQKFIALFYT 300

QY 301 VVTPALNPLIYTLRNTVEKSAHRHMVLENCSSAGKLAQI 340  
 DB 301 VVTPALNPLIYTLRNTVEKSAHRHMVLENCSSAGKLAQI 340

## RESULT 3

AAU24748  
 ID AAU24748 standard; protein; 340 AA.  
 XX  
 AC AAU24748;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human olfactory receptor AOLF248.  
 XX  
 KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;  
 KW food additive; cosmetic; fragrance; pharmaceutical additive.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200168805-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 13-MAR-2001; 2001WO-US007771.  
 XX  
 PR 13-MAR-2000; 2000US-0188914P.  
 PR 24-MAR-2000; 2000US-0192033P.  
 PR 12-APR-2000; 2000US-0198474P.  
 PR 24-APR-2000; 2000US-0199335P.  
 PR 26-MAY-2000; 2000US-0207702P.  
 PR 23-JUN-2000; 2000US-0213849P.  
 PR 16-AUG-2000; 2000US-0226534P.  
 PR 07-SEP-2000; 2000US-0230732P.  
 PR 07-FEB-2001; 2001US-0266862P.  
 XX  
 PA (SENO-) SENOMYX INC.  
 XX  
 PI Zozulya S;  
 XX  
 DR WPI; 2001-570867/64.  
 DR N-PSDB; AAS42441.

XX Nucleic acids encoding human olfactory G protein-coupled receptors, where  
PT useful for screening for compounds involved in olfactory sensation, where  
PT the compounds can be used in the food, pharmaceutical and cosmetic  
PT industries to customize odors.  
XX  
XX Claim 60; Page 188; 319pp; English.  
XX  
XX The invention relates to nucleic acids encoding human olfactory  
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's  
CC specifically recognise molecules, odourants, that elicit specific  
CC olfactory sensation. The human olfactory receptors and polynucleotides  
CC encoding them are useful for screening a library of chemical compounds  
CC for compounds that are involved in olfactory sensation. Modulators of  
CC their activity are useful for pharmacological and genetic modulation of  
CC olfactory signalling pathways. Therefore, they can be used in the food,  
CC pharmaceutical and cosmetic industries to customise odours and  
CC fragrances. The present sequence is a human olfactory receptor of the  
CC invention  
XX  
XX Sequence 340 AA;  
XX  
XX Query Match 99.5%; Score 1767; DB 4; Length 340;  
XX Best Local Similarity 99.4%; Pred. No. 2.5e-186;  
XX Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 1 MPCMPCALPTGGLLPHQHTMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMWISI 60  
XX DB 1 MPCMPCALPTGGLLPHQHTMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMWISI 60  
XX  
XX QY 61 LGNGIILVSHDTHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120  
XX DB 61 LGNGIILVSHDTHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120  
XX  
XX QY 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
XX DB 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
XX  
XX QY 181 STUTMLPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYG 240  
XX DB 181 STUTMLPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYG 240  
XX  
XX QY 241 HIARAVLKIRSAEGRKAFNCTSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYT 300  
XX DB 241 HIARAVLKIRSAEGRKAFNCTSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYT 300  
XX  
XX QY 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI 340  
XX DB 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI 340  
XX  
XX RESULT 4  
XX AAU85368  
XX ID AAU85368 standard; protein; 340 AA.  
XX  
XX AC AAU85368;  
XX  
XX XX 08-MAY-2002 (first entry)  
XX  
XX DE G-coupled olfactory receptor #229.  
XX  
XX Human; olfactory G-coupled receptor; sensory perception of odourant;  
XX odour composition; taste composition.  
XX  
XX OS Homo sapiens.  
XX  
XX PN W0200198526-A2.  
XX  
XX PD 27-DEC-2001.  
XX  
XX XX 22-JUN-2001; 2001WO-US020122.  
XX  
XX XX 22-JUN-2000; 2000US-0213812P.

PR 13-MAR-2001; 2001US-00804291.  
XX  
XX (SENO-) SENOMYX INC.  
XX  
XX Zozulya S, Stryer L;  
XX  
XX WPI; 2002-083330/11.  
XX N-PSDB; ABK37727.  
XX  
XX Representing sensory perception of one or more odorants for the  
PT identification and design of tastes and odors comprises providing a  
PT representative group of n olfactory receptors.  
XX  
XX Claim 1; Page 162; 182pp; English.  
XX  
XX The invention relates to a method of representing sensory perception of  
CC one or more odorants. The method comprises: (a) providing a  
CC representative class of n olfactory receptors or ligand binding domains  
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of  
CC at least one activity of one or more odorants selected from: (i) binding  
CC one or more odorants to the LBD of at least one of the n olfactory  
CC receptors; (ii) activating at least one of the n olfactory receptors with  
CC the one or more odorants; and (iii) blocking at least one of the n  
CC olfactory receptors with the one or more odorants; and (c) generating a  
CC representation of the sensory perception from the values X1 to Xn. The  
CC representation of the sensory perception of odorants is useful for the  
CC design and formulation of odour and taste compositions. AAU85140-AU85393  
CC represent human olfactory G-coupled receptor amino acid sequences of the  
CC invention  
XX  
XX SQ Sequence 340 AA;  
XX  
XX Query Match 99.5%; Score 1767; DB 5; Length 340;  
XX Best Local Similarity 99.4%; Pred. No. 2.5e-186;  
XX Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 1 MPCMPCALPTGGLLPHQHTMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMWISI 60  
XX DB 1 MPCMPCALPTGGLLPHQHTMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMWISI 60  
XX  
XX QY 61 LGNGIILVSHDTHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120  
XX DB 61 LGNGIILVSHDTHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120  
XX  
XX QY 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
XX DB 121 QFYISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
XX  
XX QY 181 STUTMLPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYG 240  
XX DB 181 STUTMLPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYG 240  
XX  
XX QY 241 HIARAVLKIRSAEGRKAFNCTSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYT 300  
XX DB 241 HIARAVLKIRSAEGRKAFNCTSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYT 300  
XX  
XX QY 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI 340  
XX DB 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI 340  
XX  
XX RESULT 5  
XX ABR63707  
XX ID ABR63707 standard; protein; 337 AA.  
XX  
XX AC ABR63707;  
XX  
XX XX 29-SEP-2003 (first entry)  
XX  
XX DE Human G-protein coupled receptor BCA-GPCR3-B.  
XX  
XX KW Human; G-protein coupled receptor; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3;  
XX BCA-GPCR-4; breast cancer; cytostatic; cancer; prostate cancer.

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XX OS Homo sapiens.
XX PN WO2003054542-A1.
XX PD 03-JUL-2003.
XX PF 18-DEC-2002; 2002WO-US041112.
XX PR 20-DEC-2001; 2001US-00028521.
XX PA (TULA-) TULARIK INC.
XX PI Powers S, Yang J, Cutler G;
XX WPI; 2003-569288/53.
XX DR N-PSDB; ACC85515.
XX PT New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,
XX PT useful for treating cancer, e.g. breast or prostate cancer.
XX PS Claim 10; Page 64; 77pp; English.
XX CC The present invention provides the protein and coding sequences of four
XX CC novel human G-protein coupled receptors (GPCR) which are amplified in
XX CC breast cancers. The sequences are useful in the treatment of cancers,
XX CC including breast and prostate cancers. The present sequence is a GPCR of
XX CC the invention
XX SQ Sequence 337 AA;
Query Match 98.8%; Score 1755; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.3e-185;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MPCALPTGGLPHQPTWMEIANVSSPEVFLVLLGFSARPSETLVLFIVLVSFYMVSIIGN 63
DB 1 MPCALPTGGLPHQPTWMEIANVSSPEVFLVLLGFSARPSETLVLFIVLVSFYMVSIIGN 60
QY 64 GIIILVSHDTHLTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVVQFY 123
DB 61 GIIILVSHDTHLTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVVQFY 120
QY 124 ISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTL 183
DB 121 ISHWLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTL 180
QY 184 TMLPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIA 243
DB 181 TMLPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIA 240
QY 244 RAVLKIRSAEGRRKAFNFTCSSHVAVVSIFYGSIIFMYLQPAKSTSHQGFIALFYTVVT 303
DB 241 RAVLKIRSAEGRRKAFNFTCSSHVAVVSIFYGSIIFMYLQPAKSTSHQGFIALFYTVVT 300
QY 304 PALNPLYTLNTEVKSAALRHVMVLENC CGSAGKLAQI 340
DB 301 PALNPLYTLNTEVKSAALRHVMVLENC CGSAGKLAQI 337
RESULT 6
ABP95893
ID ABP95893 standard; protein; 377 AA.
XX AC ABP95893;
XX DT 06-MAR-2003 (first entry)
XX DE Human GPCR polypeptide SEQ ID NO 596.
XX KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
XX KW drug development; gustatory; taste; fragrance; receptor.

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OS Homo sapiens.
XX PN WO200216548-A2.
XX PD 28-FEB-2002.
XX PF 30-JUL-2001; 2001WO-IB001446.
XX PR 04-AUG-2000; 2000JP-00237818.
XX PR 13-FEB-2001; 2001JP-00034434.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Haga T, Takeda S, Mitaku S;
XX WPI; 2002-304118/34.
XX DR N-PSDB; ABZ43167.
XX PT Database global search for G protein-coupled receptors, proteins and
XX PT encoded genes for studying in vivo signal transduction mechanism and
XX PT identifying targets for drug development.
XX PS Claim 10; SEQ ID NO 596; 97pp + Sequence Listing; Japanese.
XX CC The invention relates to a method for screening G protein-coupled
XX CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
XX CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
XX CC domains with 250-1000 amino acid residues to give a gene homologous with
XX CC a known GPCR gene. The receptor proteins and encoded genes are useful for
XX CC studying in vivo signal transduction mechanism and identifying targets
XX CC for drug development e.g. based on olfactory and gustatory receptors in
XX CC form of agonists and antagonists by screening intrinsic and extrinsic
XX CC ligands as bitter taste inhibitors, taste enhancers and fragrance
XX CC improvers. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at fcp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 377 AA;
Query Match 97.1%; Score 1725; DB 5; Length 377;
Best Local Similarity 99.4%; Pred. No. 1.3e-181;
Matches 332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 ALPTGGLPHQPTWMEIANVSSPEVFLVLLGFSARPSETLVLFIVLVSFYMVSIIGNGII 66
DB 44 ALPTGGLPHQPTWMEIANVSSPEVFLVLLGFSARPSETLVLFIVLVSFYMVSIIGNGII 103
QY 67 ILVSHDTHLTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVVQFYISH 126
DB 104 ILVSHDTHLTPMYFFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVVQFYISH 163
QY 127 WLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTLTM 186
DB 164 WLGATECVLLATMSYDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTLTM 223
QY 187 LPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIA 246
DB 224 LPLCGNCCIDHFFCEMPLIMOLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIA 283
QY 247 LKIRSAEGRRKAFNFTCSSHVAVVSIFYGSIIFMYLQPAKSTSHQGFIALFYTVVT 306
DB 284 LKIRSAEGRRKAFNFTCSSHVAVVSIFYGSIIFMYLQPAKSTSHQGFIALFYTVVT 343
QY 307 NPLIYTLNTEVKSAALRHVMVLENC CGSAGKLAQI 340
DB 344 NPLIYTLNTEVKSAALRHVMVLENC CGSAGKLAQI 377
RESULT 7
ABR63708
ID ABR63708 standard; protein; 320 AA.
XX AC ABR63708;

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CC transgenic animals for studying the function and/or activity of GPCR  
 CC protein and for identifying and/or evaluating modulators of GPCR protein  
 CC activity. This is the amino acid sequence of a novel G-protein coupled  
 CC receptor described in the invention  
 XX  
 SQ Sequence 320 AA;

Query Match 93.0%; Score 1651; DB 5; Length 320;  
 Best Local Similarity 99.7%; Pred. No. 1.6e-173;  
 Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 21 MMEIANVSSPEVLLGFSARPSLETVLFIIVLSPFVMSILGNGIIILVSHTDVHLTPM 80  
 DB 1 MMEIANVSSPEVLLGFSARPSLETVLFIIVLSPFVMSILGNGIIILVSHTDVHLTPM 60

QY 81 YFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVQFYISHWLGATECVLLATMS 140  
 DB 61 YFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVQFYISHWLGATECVLLATMS 120

QY 141 YDYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 200  
 DB 121 YDYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 180

QY 201 EMPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAVAVLKIRSAEGRKAFN 260  
 DB 181 EMPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAVAVLKIRSAEGRKAFN 240

QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALEFYVTVPALNPLIYTLNTEVKS 320  
 DB 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALEFYVTVPALNPLIYTLNTEVKS 300

QY 321 ALRHMVLENCSSAGKLAQI 340  
 DB 301 ALRHMVLENCSSAGKLAQI 320

## RESULT 9

ABR63709  
 ID ABR63709 standard; protein; 319 AA.

AC ABR63709;

DT 29-SEP-2003 (first entry)

XX Human G-protein coupled receptor BCA-GPCR3-D.

XX Human; G-protein coupled receptor; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3;  
 KW BCA-GPCR-4; breast cancer; cytostatic; cancer; prostate cancer.

XX Homo sapiens.

OS WO2003054542-A1.

PN 03-JUL-2003.

XX 18-DEC-2002; 2002WO-US041112.

XX 20-DEC-2001; 2001US-00028521.

XX (TULA-) TULARIK INC.

XX Powers S, Yang J, Cutler G;

XX WPI; 2003-569288/53.

XX N-PSDB; ACC85517.

XX New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,  
 PT useful for treating cancer, e.g. breast or prostate cancer.

XX Claim 10; Page 66; 77pp; English.

XX The present invention provides the protein and coding sequences of four  
 CC novel human G-protein coupled receptors (GPCR) which are amplified in

CC breast cancers. The sequences are useful in the treatment of cancers,  
 CC including breast and prostate cancers. The present sequence is a GPCR of  
 CC the invention

XX SQ Sequence 319 AA;

Query Match 92.8%; Score 1649; DB 6; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-173;  
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 MEIANVSSPEVLLGFSARPSLETVLFIIVLSPFVMSILGNGIIILVSHTDVHLTPMY 81  
 DB 1 MEIANVSSPEVLLGFSARPSLETVLFIIVLSPFVMSILGNGIIILVSHTDVHLTPMY 60

QY 82 YFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVQFYISHWLGATECVLLATMSY 141  
 DB 61 YFLANLSFLDMSFTTSIVPOLLANLWGPQKTSYGGCVQFYISHWLGATECVLLATMSY 120

QY 142 DYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 201  
 DB 121 DYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 180

QY 202 MPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAVAVLKIRSAEGRKAFN 261  
 DB 181 MPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAVAVLKIRSAEGRKAFN 240

QY 262 CSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALFYVTVPALNPLIYTLNTEVKS 321  
 DB 241 CSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALFYVTVPALNPLIYTLNTEVKS 300

QY 322 LRHMVLENCSSAGKLAQI 340  
 DB 301 LRHMVLENCSSAGKLAQI 319

## RESULT 10

ABJ04731  
 ID ABJ04731 standard; protein; 320 AA.

AC ABJ04731;

DT 16-OCT-2002 (first entry)

XX GPCR 11 protein SEQ ID No 28.

XX Antidiabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCR;  
 KW antiparkinsonian; cardiant; antiarteriosclerotic; immunosuppressive;  
 KW hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory;  
 KW anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;  
 KW diabetes; metabolic disorder; diabetes; obesity; infectious disease;  
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia;  
 KW Parkinson's disorder; immune disorder; haematopoietic disorder; obesity;  
 KW metabolic syndrome X; wasting disorder; cancer; hypertension; lymphoma;  
 KW congenital heart defect; aortic stenosis; subaortic stenosis; neoplasm;  
 KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;  
 KW prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;  
 KW hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;  
 KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;  
 KW multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;  
 KW gene therapy; transgenic animal.

XX Unidentified.

XX WO200246229-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US046530.

XX 05-DEC-2000; 2000US-0251459P.

XX 29-DEC-2000; 2000US-0259007P.

XX 04-DEC-2001; 2001US-00005041.

(CURA-) CURAGEN CORP.

PA Corman SJ, Padigar M, Burgess CE, Shimkets RA, Spytek KA;  
PI Gilbert JA, Mayotte JE, Baumgartner JC, Mishra V, Vernet CAM;  
PI Dickinson KS, Ballinger RA, Wolenc AR;  
XX WPI: 2002-537559/57.  
DR N-PSDB; ABO5662.  
XX Novel isolated G-protein coupled receptor polypeptide, designated NOVX,  
PT useful for treating or preventing in human receptor-associated disorders  
PT e.g. cardiomyopathy, atherosclerosis or diabetes.  
XX Claim 1; Page 69; 264pp; English.

CC The invention relates to a novel isolated G-protein coupled receptor X  
CC (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide  
CC and the antibody of the isolated protein is useful for treating or  
CC preventing a GPCRX-associated disorder in a subject, preferably human,  
CC where the disorder is cardiomyopathy, atherosclerosis or diabetes. The  
CC isolated protein, its encoding polynucleotide and the antibody of the  
CC isolated protein is useful for treating or preventing metabolic  
CC disorders, diabetes, obesity, infectious disease, anorexia,  
CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,  
CC immune disorders, haematopoietic disorders, and various dyslipidaemias, X,  
CC metabolic disturbances associated with obesity, the metabolic syndrome X,  
CC wasting disorders associated with chronic diseases, and cancer. The  
CC disorders also include cardiomyopathy, atherosclerosis, hypertension,  
CC congenital heart defects, aortic stenosis, subaortic stenosis,  
CC transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia,  
CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,  
CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic  
CC purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial  
CC asthma, Crohn's disease, and multiple sclerosis. The isolated protein,  
CC its encoding polynucleotide and the antibody of the isolated protein is  
CC useful in screening assays, detection assays (e.g., chromosomal mapping,  
CC tissue typing, forensic biology). The isolated polynucleotide is useful  
CC in gene therapy, to express the isolated protein, to detect GPCRX mRNA or  
CC a genetic lesion in a GPCRX gene, and to modulate GPCRX activity. The  
CC cell of the invention is useful for producing non-human transgenic  
CC animals. This sequence represents a GPCRX protein of the invention  
XX  
SQ Sequence 320 AA;

Query Match 92.7%; Score 1646; DB 5; Length 320;  
Best Local Similarity 99.4%; Pred. No. 5.6e-173;  
Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 21 MMEIANVSSPEVFLGFSARPSLETVLFIVVLFSFYMVSILGNGIILVSHDTHLTPM 80  
DB 1 MMEIANVSSPEVFLGFSARPSLETVLFIVVLFSFYMVSILGNGIILVSHDTHLTPM 60  
QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVQVFIYSHWLGATECVLLATMS 140  
DB 61 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVQVFIYSHWLGATECVLLATMS 120  
QY 141 YDRAAICRPLHYVTVMHPOLCLGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFC 200  
DB 121 YDRAAICRPLHYVTVMHPOLCLGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFC 180  
QY 201 EMPLIMQLACVDTSLNEMEMYLASFVFWVLPLGLILVSYGHIAARAVLKIRSAEGRKAFN 260  
DB 181 EMPLIMQLACVDTSLNEMEMYLASFVFWVLPLGLILVSYGHIAARAVLKIRSAEGRKAFN 240  
QY 261 TCSSHAVVSLFYGSIIIFMYLQPAKSTSHQGFIALFYVTVPALNPLYTLNTEVKS 320  
DB 241 TCSSHAVVSLFYGSIIIFMYLQPAKSTSHQGFIALFYVTVPALNPLYTLNTEVKS 300  
QY 321 ALRHMVLENCSSAGKLAQI 340  
DB 301 ALRHMVLENCSSAGKLAQI 320

RESULT 11

ADC86041  
ID ADC86041 standard; protein; 320 AA.  
XX AC  
AC ADC86041;  
XX DT  
DT 01-JAN-2004 (first entry)  
XX DE  
DE Human GPCR protein SEQ ID NO:494.  
XX KW  
KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
KW gene therapy.  
XX OS  
OS Homo sapiens.  
XX PN  
PN EP1270724-A2.  
XX PD  
PD 02-JAN-2003.  
XX PF  
PF 18-JUN-2002; 2002EP-00013517.  
XX PR  
PR 18-JUN-2001; 2001JP-00246789.  
XX PA  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
XX PI  
PI Suwa M, Asai K, Akiyama Y, Aburatani H;  
XX WPI; 2003-315783/31.  
XX N-PSDB; ADC86040.  
XX PT  
PT New polynucleotide, useful for preparing a composition for treating a  
PT patient in need of increased or suppressed activity or expression of the  
PT guanosine triphosphate-binding protein coupled receptor.  
XX PS  
PS Claim 2; SEQ ID NO 494; 28pp; English.  
XX CC  
CC The invention relates to a novel polynucleotide encoding a guanosine  
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
CC the invention may have a use in gene therapy. The polynucleotide and  
CC polypeptide are useful for preparing a composition for treating a patient  
CC in need of increased or suppressed activity or expression of the  
CC guanosine triphosphate-binding protein coupled receptor. The protein  
CC sequences shown in ADC8549-ADC87617 represent GPCR's of the invention.  
XX SQ  
SQ Sequence 320 AA;  
Query Match 92.6%; Score 1645; DB 7; Length 320;  
Best Local Similarity 99.4%; Pred. No. 7.2e-173;  
Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 21 MMEIANVSSPEVFLGFSARPSLETVLFIVVLFSFYMVSILGNGIILVSHDTHLTPM 80  
DB 1 MMEIANVSSPEVFLGFSARPSLETVLFIVVLFSFYMVSILGNGIILVSHDTHLTPM 60  
QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVQVFIYSHWLGATECVLLATMS 140  
DB 61 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVQVFIYSHWLGATECVLLATMS 120  
QY 141 YDRAAICRPLHYVTVMHPOLCLGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFC 200  
DB 121 YDRAAICRPLHYVTVMHPOLCLGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFC 180  
QY 201 EMPLIMQLACVDTSLNEMEMYLASFVFWVLPLGLILVSYGHIAARAVLKIRSAEGRKAFN 260  
DB 181 EMPLIMQLACVDTSLNEMEMYLASFVFWVLPLGLILVSYGHIAARAVLKIRSAEGRKAFN 240  
QY 261 TCSSHAVVSLFYGSIIIFMYLQPAKSTSHQGFIALFYVTVPALNPLYTLNTEVKS 320  
DB 241 TCSSHAVVSLFYGSIIIFMYLQPAKSTSHQGFIALFYVTVPALNPLYTLNTEVKS 300  
QY 321 ALRHMVLENCSSAGKLAQI 340  
DB 301 ALRHMVLENCSSAGKLAQI 320

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Db      301 ALRHMVLECCSGSAGKLAQI 320
RESULT 12
AAG71912
ID      AAG71912 standard; protein; 319 AA.
XX      AC      AAG71912;
XX      XX      30-JUL-2001 (first entry)
XX      DT      Human olfactory receptor polypeptide, SEQ ID NO: 1593.
XX      DE      Human; olfactory receptor; OR; primary scent determination;
XX      KW      secondary scent determination; polypeptide library; odour receptor;
XX      KW      scent profile; scent fingerprint; scent representation.
XX      OS      Homo sapiens.
XX      XX      WO200127158-A2.
XX      PN      19-APR-2001.
XX      PD      06-OCT-2000; 2000WO-US027582.
XX      PF      08-OCT-1999; 99US-0158615P.
XX      PR      24-FEB-2000; 2000US-0184809P.
XX      XX      (DIGI-) DIGISCENTS.
XX      PA      (YEDA ) YEDA RES & DEV CO LTD.
XX      PI      Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX      DR      WPI; 2001-290713/30.
XX      PT      New polynucleotides which encode polypeptides involved in olfactory
XX      PT      sensation for identifying olfactory agonists and antagonists.
XX      PS      Claim 11; Page 1029-1030; 1857pp; English.
XX      CC      The present sequence is an olfactory receptor which is encoded by one of
XX      CC      a number of novel polynucleotides. The polynucleotides can be used in
XX      CC      screening for olfactory agonists and antagonists. The methods allow for
XX      CC      the determination of primary scents and the identification of the odour
XX      CC      receptors used to detect these primary scents. The methods also enable
XX      CC      determination of secondary scents and the identification of combinations
XX      CC      of odour receptors that are involved in detecting such secondary scents.
XX      CC      This enables the construction of a scent representation (also called a
XX      CC      scent fingerprint or scent profile), which may be used to re-create and
XX      CC      edit scents. Libraries of olfactory receptors are useful for determining
XX      CC      the interaction pattern of a composition with the receptors, and can be
XX      CC      used for determining differences in the olfactory faculties of different
XX      CC      individuals
XX      SQ      Sequence 319 AA;
Query Match      92.4%; Score 1641; DB 4; Length 319;
Best Local Similarity 99.4%; Pred. No. 2e-172;
Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      21 MMEIANVSSPEVFLGFSARPSLETVLFIWLSFYVMSILGNGIILVSHTDVHLHTPM 80
Db      1 MMEIANVSSPEVFLGFSRPSLETVLFIWLSFYVMSILGNGIILVSHTDVHLHTPM 60
Qy      81 YFFLANLSFLDMSTTSIVPOLLANLWGPQKTSYGGCVVQFYISHWLGATECVLATMS 140
Db      61 YFFLANLPFFDMSTTSIVPOLLANLWGPQKTSYGGCVVQFYISHWLGATECVLATMS 120
Qy      141 YDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTLTMLPLCGNCCIDHFFC 200
Db      121 YDRAAICRPLHYTVIMHPOLCLGLALASWLGGLTTSWVGSTLTMLPLCGNCCIDHFFC 180
Qy      201 EMPLIMQLACVDTSLNEMEMYLASFVFWVLPLGLILVSYGHIAKIRSAEGRRKAFN 260
181 EMPLIMQLACVDTSLNEMEMYLASFVFWVLPLGLILVSYGHIAKIRSAEGRRKAFN 240
261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLRNTVKS 320
241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLRNTVKS 300
321 ALRHMVLECCSGSAGKLAQ 339
301 ALRHMVLECCSGSAGKLAQ 319
RESULT 13
AAG71896
ID      AAG71896 standard; protein; 319 AA.
XX      AC      AAG71896;
XX      XX      30-JUL-2001 (first entry)
XX      DT      Human olfactory receptor polypeptide, SEQ ID NO: 1577.
XX      DE      Human; olfactory receptor; OR; primary scent determination;
XX      KW      secondary scent determination; polypeptide library; odour receptor;
XX      KW      scent profile; scent fingerprint; scent representation.
XX      OS      Homo sapiens.
XX      XX      WO200127158-A2.
XX      PN      19-APR-2001.
XX      PD      06-OCT-2000; 2000WO-US027582.
XX      PF      08-OCT-1999; 99US-0158615P.
XX      PR      24-FEB-2000; 2000US-0184809P.
XX      XX      (DIGI-) DIGISCENTS.
XX      PA      (YEDA ) YEDA RES & DEV CO LTD.
XX      PI      Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX      DR      WPI; 2001-290713/30.
XX      PT      New polynucleotides which encode polypeptides involved in olfactory
XX      PT      sensation for identifying olfactory agonists and antagonists.
XX      PS      Claim 11; Page 1016; 1857pp; English.
XX      CC      The present sequence is an olfactory receptor which is encoded by one of
XX      CC      a number of novel polynucleotides. The polynucleotides can be used in
XX      CC      screening for olfactory agonists and antagonists. The methods allow for
XX      CC      the determination of primary scents and the identification of the odour
XX      CC      receptors used to detect these primary scents. The methods also enable
XX      CC      determination of secondary scents and the identification of combinations
XX      CC      of odour receptors that are involved in detecting such secondary scents.
XX      CC      This enables the construction of a scent representation (also called a
XX      CC      scent fingerprint or scent profile), which may be used to re-create and
XX      CC      edit scents. Libraries of olfactory receptors are useful for determining
XX      CC      the interaction pattern of a composition with the receptors, and can be
XX      CC      used for determining differences in the olfactory faculties of different
XX      CC      individuals
XX      SQ      Sequence 319 AA;
Query Match      92.4%; Score 1641; DB 4; Length 319;
Best Local Similarity 99.4%; Pred. No. 2e-172;
Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      21 MMEIANVSSPEVFLGFSARPSLETVLFIWLSFYVMSILGNGIILVSHTDVHLHTPM 80
Db      1 MMEIANVSSPEVFLGFSRPSLETVLFIWLSFYVMSILGNGIILVSHTDVHLHTPM 60

```

QY 81 YFFLANLSFLDMSFTTIVPOLLANLWGPQKTSYGGCVQVYISHWLGATECVLLATMS 140  
 DB |||||  
 QY 141 YDRAAICRPLHYTVIMHPQCLGLALASWLGGLTTSVMGSLTMLLPLCGNCCIDHFFC 200  
 DB |||||  
 QY 121 YDRAAICRPLHYTVIMHPQCLGLALASWLGGLTTSVMGSLTMLLPLCGNCCIDHFFC 180  
 DB |||||  
 QY 201 EMPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAVAVLKIRSAEGRRAFN 260  
 DB |||||  
 QY 181 EMPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAVAVLKIRSAEGRRAFN 240  
 DB |||||  
 QY 261 TCSSHVAVSLFYGSIIFMYLQPAKSTSHQCKFIALFYVTPALNPLIYTLRNTVEKS 320  
 DB |||||  
 QY 241 TCSSHVAVSLFYGSIIFMYLQPAKSTSHQCKFIALFYVTPALNPLIYTLRNTVEKS 300  
 DB |||||  
 QY 321 ALRHMVLENCSSAGKLAQ 339  
 DB |||||  
 QY 301 ALRHMVLENCSSAGKLAQ 319  
 DB |||||

RESULT 14  
 ABU11186  
 ID ABU11186 standard; protein; 319 AA.  
 AC ABU11186;  
 XX  
 DT 06-FEB-2003 (first entry)  
 XX  
 DE Human G-protein coupled receptor GCRC-39.  
 XX  
 DE Human; G-protein coupled receptor; GPCR; GCRC; INTSIG; cancer;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;  
 KW diabetes; Grave's disease; leukaemia; cervical cancer; breast cancer;  
 KW immunological disorder; scleroderma; systemic lupus erythematosus;  
 KW allergy; gastrointestinal disorder; Crohn's disease; renal disorder;  
 KW Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic;  
 KW protozoal; helminthic; cardiovascular disorder; atherosclerosis;  
 KW hepatic disease; cirrhosis; transgenic; neuroprotective; relaxant;  
 KW antihypertoid; cycostatic; dermatological; immunosuppressive; uteropath;  
 KW thyromimetic; antiinflammatory; cerebroprotective; gastrointestinal;  
 KW hepatotropic; nephrotropic; anticonvulsant; antirheumatic; cardiac;  
 KW nootropic; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200279448-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 29-MAR-2002; 2002WO-US0009923.  
 XX  
 PF 30-MAR-2001; 2001US-0280683P.  
 PR 13-APR-2001; 2001US-0283714P.  
 PR 20-APR-2001; 2001US-0285336P.  
 PR 27-APR-2001; 2001US-0287266P.  
 XX  
 PA (INCYTE) INCYTE GENOMICS INC.  
 XX  
 PI Thornton M, Yao MG, Richardson TW, Swarnakar A, Kallick DA;  
 PI Ison CH, Walia NK, Gandhi AR, Lee EA, Elliott VS, Hafalia AJA;  
 PI Au-Young J, Griffin JA, Baughn MR, Khan FA, Becha S, Lu Y;  
 PI Arvizu CP, Borowsky ML, Lal PG, Ramkumar J, Emerling BM, Walsh RT;  
 PI Yue H, Burford N, Graul RC;  
 XX  
 DR WPI; 2003-058430/05.  
 DR N-PSDB; ABX17885.  
 XX  
 PT New GCRC polypeptides, useful for diagnosing, preventing, and treating  
 disorders associated with an abnormal expression or activity of GCRC,  
 e.g. neuromuscular, immunological, cardiovascular disorders, cancer and  
 infection.

XX  
 PS Claim 1; Page 236-237; 313pp; English.  
 XX  
 CC The present invention relates to the isolation of human G-protein coupled  
 CC receptors (GPCRs, designated GCRC), and the polynucleotide sequences  
 CC encoding them. The GCRC polypeptides or their fragments, and the  
 CC polynucleotide sequences encoding them are useful in diagnosing,  
 CC preventing, and treating disorders associated with an abnormal expression  
 CC or activity of INTSIG, such as neurodegenerative disorders (e.g.  
 CC Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.  
 CC myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes,  
 CC Grave's disease), cancers (e.g. leukaemia, cervical or breast cancers),  
 CC immunological disorders (e.g. scleroderma, systemic lupus erythematosus,  
 CC allergies), gastrointestinal disorders (e.g. Crohn's disease), renal  
 CC disorders (e.g. Goodpasture's syndrome), infections (e.g. viral,  
 CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular  
 CC disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis).  
 CC GCRC or its fragments may also be used in screening for compounds that  
 CC specifically bind to and modulate the activity of GCRC. The  
 CC polynucleotides can be used to create humanised animals or transgenic  
 CC animals to model human disease. ABU1148-ABU11220 represent the human  
 CC GCRCs of the invention  
 XX  
 SQ Sequence 319 AA;  
 Query Match 92.3%; Score 1640; DB 6; Length 319;  
 Best Local Similarity 99.4%; Pred. No. 2.6e-172;  
 Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 22 MEIANVSSPEVFLVLLGFSARPSLETVLFIVLVSFYMSILGNGIILVSHVTDVHLHTPMY 81  
 DB |||||  
 QY 82 FFLANLSFLDMSFTTIVPOLLANLWGPQKTSYGGCVQVYISHWLGATECVLLATMSY 141  
 DB |||||  
 QY 61 FFLANLPFLDMSFTTIVPOLLANLWGPQKTSYGGCVQVYISHWLGATECVLLATMSY 120  
 DB |||||  
 QY 142 DRYAATCRPLHYTVIMHPQCLGLALASWLGGLTTSVMGSLTMLLPLCGNCCIDHFFCE 201  
 DB |||||  
 QY 121 DRYAATCRPLHYTVIMHPQCLGLALASWLGGLTTSVMGSLTMLLPLCGNCCIDHFFCE 180  
 DB |||||  
 QY 202 MPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAVAVLKIRSAEGRRAFN 261  
 DB |||||  
 QY 181 MPLIMOLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAVAVLKIRSAEGRRAFN 240  
 DB |||||  
 QY 262 CSSHVAVSLFYGSIIFMYLQPAKSTSHQCKFIALFYVTPALNPLIYTLRNTVEKSA 321  
 DB |||||  
 QY 241 CSSHVAVSLFYGSIIFMYLQPAKSTSHQCKFIALFYVTPALNPLIYTLRNTVEKSA 300  
 DB |||||  
 QY 322 LRHMVLENCSSAGKLAQI 340  
 DB |||||  
 QY 301 LRHMVLENCSSAGKLAQI 319  
 DB |||||

RESULT 15  
 ABG76850  
 ID ABG76850 standard; protein; 314 AA.  
 XX  
 AC ABG76850;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human G-protein coupled receptor (GPCR) protein #84.  
 XX  
 KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;  
 KW diabetes; cell signal processing; metabolic pathway modulation; cancer;  
 KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;  
 KW immune response; neurodegenerative disorder; inflammatory disorder;  
 KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;  
 KW receptor.  
 XX  
 OS Homo sapiens.

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PN WO200259313-A2.
XX 01-AUG-2002.
XX 18-DEC-2001; 2001WO-US049394.
XX 18-DEC-2000; 2000US-0256635P.
XX 21-DEC-2000; 2000US-0257876P.
XX 04-JAN-2001; 2001US-0259743P.
XX 10-JAN-2001; 2001US-0260718P.
XX 12-JAN-2001; 2001US-0261498P.
XX 24-JAN-2001; 2001US-0263689P.
XX 08-FEB-2001; 2001US-0267464P.
XX 22-FEB-2001; 2001US-0271021P.
XX 14-MAR-2001; 2001US-0275946P.
XX 23-MAR-2001; 2001US-0278150P.
XX 18-APR-2001; 2001US-0284591P.
XX 23-APR-2001; 2001US-0285718P.
XX 19-JUN-2001; 2001US-0299327P.
XX 16-AUG-2001; 2001US-0312902P.
XX (CURA-) CURAGEN CORP.
XX Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Casman SJ, Vernet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S;
PI Gerlach V, Smithson G, Stone DJ, Sciore P, Macdougall JR, Gunther E;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX WPI; 2002-599789/64.
DR N-PSDB; ABS58830.
XX
XX New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.
XX
XX Claim 9; Page 166; 685pp; English.
XX
XX The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterus cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Albrit hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. ABG76767-ABG76870 represent human
CC GPCR amino acid sequences of the invention
XX
XX Sequence 314 AA;

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Query Match 91.0%; Score 1617; DB 5; Length 314;
Best Local Similarity 99.4%; Pred. No. 8.e-170;
Matches 312; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 21 MMEIANVSSPEVFLGFSARPSLETFLVLVSFTYVSVILNGNIIILVSHVTDVHLHTPM 80
DB 1 MMEIANVSSPEVFLGFSRPSLETFLVLVSFTYVSVILNGNIIILVSHVTDVHLHTPM 60
QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPKTISYGGCVVQVFYISHWLGCATCVLLATMS 140
DB 61 YFFLANLPFLDMSFTTSIVPQLLANLWGPKTISYGGCVVQVFYISHWLGCATCVLLATMS 120

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QY 141 YDRAAICRPLHYTVINHPQLCLGLALASWLGGLTTSWVGSTLTMLPLCGNNCIDHFFC 200
DB 121 YDRAAICRPLHYTVINHPQLCLGLALASWLGGLTTSWVGSTLTMLPLCGNNCIDHFFC 180
QY 201 EMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIARAVLKIRASGRRKAFN 260
DB 181 EMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIARAVLKIRASGRRKAFN 240
QY 261 TCSSHVAVVSFLFYGSIIIFYLQPAKSTSHQGFIALFYTVVTPALNPLIYTLRNTKVS 320
DB 241 TCSSHVAVVSFLFYGSIIIFYLQPAKSTSHQGFIALFYTVVTPALNPLIYTLRNTKVS 300
QY 321 ALRHWLENC CGSA 334
DB 301 ALRHWLENC CGSA 314

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Search completed: April 8, 2005, 17:08:27  
Job time : 176 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:54:13 ; Search time 46 Seconds  
(without alignments)  
711.167 Million cell updates/sec

Title: US-10-633-894-6  
Perfect score: 1776  
Sequence: 1 MPCMPCALPTGGLPHPHQT.....ALRHVLENCSSAGKLAQI 340

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	985	55.5	312	2 A46247	olfactory receptor
2	868	48.9	316	2 A57069	olfactory receptor
3	769	43.3	305	2 S29711	olfactory factor 0
4	754	42.5	315	2 JC5836	olfactory receptor
5	713.5	40.2	318	2 JC5202	chemoreceptor TB64
6	682.5	38.4	313	2 S20571	olfactory receptor
7	681	38.3	314	2 S29707	olfactory receptor
8	676	38.1	313	2 B23701	olfactory receptor
9	674	38.0	319	2 JC5624	olfactory receptor
10	672	37.8	314	2 S20572	olfactory receptor
11	667	37.6	314	2 A37886	olfactory receptor
12	665	37.4	307	2 S29710	olfactory receptor
13	664	37.4	310	2 B23701	olfactory receptor
14	662	37.3	309	1 S51356	olfactory receptor
15	660	37.2	311	2 C23701	olfactory receptor
16	657	37.0	314	2 H23701	olfactory receptor
17	655	36.9	304	2 S29709	olfactory receptor
18	652	36.7	327	2 F23701	olfactory receptor
19	646	36.4	311	2 JC5200	chemoreceptor TB33
20	646	36.4	315	2 JC4658	olfactory receptor
21	644.5	36.3	312	2 A48413	probable olfactory
22	642	36.1	312	2 S29708	olfactory receptor
23	638	35.9	320	2 S20573	olfactory receptor
24	636	35.8	312	2 G23701	olfactory receptor
25	634	35.7	333	2 A23701	olfactory receptor
26	632	35.6	315	2 JC5201	chemoreceptor TB56
27	630	35.5	317	2 D23701	olfactory receptor
28	610	34.3	312	2 I23701	olfactory receptor
29	565	31.8	312	2 A46750	olfactory receptor

30	532	30.0	222	2 D40745	odorant receptor (
31	510	28.7	254	2 PC4369	olfactory receptor
32	497	28.0	222	2 B40745	odorant receptor (
33	493	27.8	157	2 S58035	probable olfactory
34	478	26.9	234	2 S29000	G protein-coupled
35	474	26.7	232	2 S29001	G protein-coupled
36	466	26.2	216	2 I38474	olfactory receptor
37	465.5	26.2	225	2 I38478	olfactory receptor
38	462	26.0	216	2 I38470	olfactory receptor
39	462	26.0	216	2 I38480	olfactory receptor
40	461.5	26.0	154	2 S58070	probable olfactory
41	455	25.6	216	2 I38476	olfactory receptor
42	452	25.5	234	2 S28998	G protein-coupled
43	450.5	25.4	328	2 G45774	odorant receptor 2
44	448	25.2	216	2 I38479	olfactory receptor
45	432	24.3	216	2 I38477	olfactory receptor

ALIGNMENTS

RESULT 1

A46247  
olfactory receptor OR3 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A46247  
R:Nef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinemann, Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992  
A:Title: Spatial pattern of receptor expression in the olfactory epithelium.  
A:Reference number: A46247, MUID:93028384; PMID:1384038  
A:Accession: A46247  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-312 <NEF>  
A:Cross-references: UNIPROT:P23275; GB:M84005; NID:G200153; PIDN:AAA39862.1; PID:G200154  
A>Note: sequence extracted from NCBI backbone (NCBIP:115362)  
C:Superfamily: olfactory receptor OR14

Query Match 55.5%; Score 985; DB 2; Length 312;  
Best Local Similarity 60.0%; Pred. No. 8.1e-77;  
Matches 183; Conservative 50; Mismatches 72; Indels 0; Gaps 0;

Qy	22	MEATANVSPEVFLLGFSARPSLETVLFIYVLSFYVMSILNGIILVSHVTDVHLHTPMY	81
Db	1	MEYDSNSSGGTFLMGVSDHPHLEIIFFAVILSYLLTLVGNLTILLSRLDARLHTPMY	60
Qy	82	FFLANLSFLDMSFTTISIVPOLLANLWGPQKTSYGGCVQFYISHMLGATECVLLATMSY	141
Db	61	FFLSNLSSLDLAFSTTSVPQMLKXNLGPDKTSYGGCVTQLYVFLWLGATECILLVVMAP	120
Qy	142	DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSWVGSTLTMLPLCGNCCIDHFCE	201
Db	121	DRYVAVCRPLHYTVVMPNRLCWGLAAISWLGGLGNSVIQSTFTLQLPFCGHRKVDNLC	180
Qy	202	MPLIMOLACVDTSLNEMEMYLASFVFLVPLGLHILSYGHIARAVLKIRSAEGRKAFNT	261
Db	181	VPAMIKLACDTSLEAVLNGVCTFTTVVPSVILSYCFIAQVAMKIRSEGRKAFNT	240
Qy	262	CSSHVAVSLFYGSIIFMYLQPAKSTSHQKGFIALFYVTPALNPLIYTLRNTKESA	321
Db	241	CVSHLVVVFYGSALYGYLLPAKSSNQSGKFSIFYSVVTMPVNPILIYTLRKEVKA	300
Qy	322	LRHMV 326	
Db	301	LGRL 305	

RESULT 2

A57069  
olfactory receptor FAT11 - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004



A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-318 <THO1>  
A:Cross-references: UNIPROT:Q62944; GB:U50949; NID:g1256392; PIDN:AA652911.1; PID:g1256392  
A:Accession: PC4304  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 145-153;245-253 <THO2>  
A:Experimental source: taste bud  
C:Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction  
C:Genetics:  
A:Gene: tb641  
C:Superfamily: olfactory receptor OR14  
C:Keywords: olfaction; taste bud; transmembrane protein  
F:30-53/Domain: transmembrane #status predicted <TM1>  
F:63-84/Domain: transmembrane #status predicted <TM2>  
F:106-125/Domain: transmembrane #status predicted <TM3>  
F:145-169/Domain: transmembrane #status predicted <TM4>  
F:202-224/Domain: transmembrane #status predicted <TM5>  
F:243-265/Domain: transmembrane #status predicted <TM6>  
F:276-296/Domain: transmembrane #status predicted <TM7>  
Query Match 40.2%; Score 713.5; DB 2; Length 318;  
Best Local Similarity 46.9%; Pred. No. 1.4e-53;  
Matches 138; Conservative 59; Mismatches 94; Indels 3; Gaps 2;  
Qy 33 FVLGFSARPSLETFLVFLVLSFVMSILNGIILVSHWLGATECVLLATMSYDRYAICRPL 151  
Db 16 FLILGLAHPNLTFLFLVFLVILYILQGLNLLITVWADPKLHARPMYILGLVLSFLD 75  
Qy 92 MSFTTSIVPOLLANLWGPQKTSYGGCVQVYISHWLGATECVLLATMSYDRYAICRPL 151  
Db 76 MLUSSVIVPRIILNFTPANKAIAFGGCVQAQLYFPHFGSTQCFLYTLMAVDYRLAICPL 135  
Qy 152 HYTIMHPQLCLGLALASWLGGLTTSVMGSLTLMPLCGNCCIDHFFCEMPLIMOLACV 211  
Db 136 RYPVLNMGKULCTILVAGAWAGSHGSIQATLTPRYCGPKEVDYFCDIPAVRLACA 195  
Qy 212 DTSLNEMMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRKAPNTCSSHVAVSL 271  
Db 196 DTAINELVTFVDIGVAASCPFLILLSYANIVHAILKIRTAGRRRAFSTCGSHLTVTVT 255  
Qy 272 FYGSIIFMYLOPAKTSHEQCKFTALFVTVTPALNPLIYTLRNTVEKSHLHMV 326  
Db 256 YYVPCIFILRAGSKSFDGA--VAVFYTVTPALNPLIYTLRNTVEKSHLHMV 307  
RESULT 6  
S20571  
olfactory receptor - dog  
C:Species: Canis lupus familiaris (dog)  
C:Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004  
C:Accession: S20571  
R:Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;  
Nature 355, 453-455, 1992  
A:Title: Expression of members of the putative olfactory receptor gene family in mammal  
A:Reference number: S20571; MUID:92131132; PMID:1370859  
A:Accession: S20571  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-313 <P>  
A:Cross-references: UNIPROT:P30955; EMBL:X64996; NID:g890; PIDN:CAA46129.1; PID:g891  
C:Superfamily: olfactory receptor OR14  
C:Keywords: G protein-coupled receptor; transmembrane protein  
Query Match 38.4%; Score 682.5; DB 2; Length 313;  
Best Local Similarity 44.6%; Pred. No. 6.2e-51;  
Matches 131; Conservative 60; Mismatches 102; Indels 1; Gaps 1;  
Qy 33 FVLGFSARPSLETFLVFLVLSFVMSILNGIILVSHWLGATECVLLATMSYDRYAICRPL 151  
Db 12 FVLGLDIDPDQDLFALFLAMVTVILGNLLIIVLIQLDLSHLTTPMYLFLSNLSFSDL 71

Qy 93 SFTTSIVPOLLANLWGPQKTSYGGCVQVYISHWLGATECVLLATMSYDRYAICRPLH 152  
Db 72 CFSVTMPKLLQNMQSQVSPISYPAGCLTQMYFFLFGDLSEFLVAMAYDRYAICRPLH 131  
Qy 153 YTIMHPQLCLGLALASWLGGLTTSVMGSLTLMPLCGNCCIDHFFCEMPLIMOLACVD 212  
Db 132 YTIMSPKLCFSLVLSVLTMPHVAHLTLLMARLFCFANT-IHPFFCDMSALLKLACSD 190  
Qy 213 TSLNEMMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRKAPNTCSSHVAVSLF 272  
Db 191 TQVNELVIFTMGGLIILVPELLIITSYARIVSSILKVPSAIGICKVFSTCGSHLSVSLF 250  
Qy 273 YGSIIFMYLOPAKTSHEQCKFTALFVTVTPALNPLIYTLRNTVEKSHLHMV 326  
Db 251 YGTVIGLYLCPNANNSTVRETIMAMMYTVTVTPMLNPFYISLRNKKMDKGAURRVI 304  
RESULT 7  
S29707  
olfactory receptor OR5 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S29707; B37286  
R:Aming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer  
Nature 361, 353-356, 1993  
A:Title: Cloning and expression of odorant receptors.  
A:Reference number: S29707; MUID:93149273; PMID:7678922  
A:Accession: S29707  
A:Molecule type: mRNA  
A:Residues: 1-314 <RAM>  
A:Cross-references: UNIPROT:Q04059  
R:Buck, L.; Axel, R.  
Cell 65, 175-187, 1991  
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od  
A:Reference number: A23701; MUID:91191556; PMID:1840504  
A:Accession: B37286  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 193-236 <BUC>  
A:Cross-references: GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:g205812  
C:Superfamily: olfactory receptor OR14  
C:Keywords: G protein-coupled receptor; membrane protein  
Query Match 38.3%; Score 681; DB 2; Length 314;  
Best Local Similarity 45.5%; Pred. No. 8.4e-51;  
Matches 133; Conservative 62; Mismatches 93; Indels 4; Gaps 2;  
Qy 33 FVLGFSARPSLETFLVFLVLSFVMSILNGIILVSHWLGATECVLLATMSYDRYAICRPLH 152  
Db 12 FLILGLDIPPEHORVFAULFSLWYLTILGNLIIILLDLSHLTTPMYLFLSNLSFSDL 71  
Qy 93 SFTTSIVPOLLANLWGPQKTSYGGCVQVYISHWLGATECVLLATMSYDRYAICRPLH 152  
Db 72 CFSVTMPKLLQNMQSQVSPISYPAGCLTQMYFFLFGDLGNFLVAMAYDRYAICRPLH 131  
Qy 153 YTIMHPQLCLGLALASWLGGLTTSVMGSLTLMPLCGNCCIDHFFCEMPLIMOLAC 210  
Db 132 YMSIMSPKLCVSLVLSWV--LTFPHAMLTLLMARLSFCEDNVIPHFCDMSALLKLAC 189  
Qy 211 VDTSLNEMMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRKAPNTCSSHVAVVS 270  
Db 190 SDTRVNEVIFIVVSFLVLPFALLIMSYRIVSSILKVPSSQGIYKAFSCGSHLSVVS 249  
Qy 271 LFYGSIIIFMYLOPAKTSHEQCKFTALFVTVTPALNPLIYTLRNTVEKSHL 322  
Db 250 LFYGTVTPILYLCFSSNNSTVKTVMSLMYTLVTPMLNPFYISLRNRDIKGM 301  
RESULT 8  
B23701  
olfactory receptor P5 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 04-Sep-1998

C;Accession: B23701  
R;Buck, L.; Axel, R.  
Cell 65, 175-187, 1991  
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od  
A;Reference number: A23701; MUID:91191556; PMID:1840504  
A;Accession: B23701  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-313 <BUC>  
A;Cross-references: GB:M64377  
C;Superfamily: olfactory receptor OR14  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 38.1%; Score 676; DB 2; Length 313;  
Best Local Similarity 45.3%; Pred. No. 2.2e-50;  
Matches 139; Conservative 57; Mismatches 107; Indels 4; Gaps 2;

QY 22 MEIANVSSPEVFLVLLGFSARPSTLVLFIVLVSYFVMSILNGIILVSHTDVHLHTPMY 81  
Db 1 MSTNQSSTVEFLLLGLSPQOQQQLFLFLIMYLATVGLNLLIILAIGTDSRLHTPMY 60

QY 82 FFLANLSFLDMGFTTSIVPOLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMSY 141  
Db 61 FFLSNLSFVDVCFSTTVPKVLNHLILGSAISPSGCLTQLYFLAVFGNMFLLAVMSY 120

QY 142 DYAAACRPLHYTVIMHPOLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFCE 201  
Db 121 DRFVALCHPLHYTVIMHPOLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFCE 180

QY 202 MPLIMQLACVDTSLNEMMYLASFVFWLPLGLHILVSYGHARAVLKIERSAEGRRKAFNT 261  
Db 181 GTPLLKLSGSDTHNELMLITFEGAVVMTVPFCILISIHITCAVLRVSSPRGKWSFST 240

QY 262 CSSHVAVVSLFYGSIIFMYLOPAKTSHEQKFI--ALFYTVVTPALNPLIYTLRNTSVK 319  
Db 241 CGSHLAVVCLFYGTGVIAYVFN--SSSLAGRDMAAAVYAVVTPMLNPFYISLRNSDMK 298

QY 320 SALRHMV 326  
Db 299 ALARKVL 305

RESULT 9  
JC5624  
olfactory receptor HTPCR92 - human  
C;Species: Homo sapiens (man)  
C;Date: 14-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: JC5624; S58003  
R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.  
Biochem. Biophys. Res. Commun. 237, 283-287, 1997  
A;Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed  
A;Reference number: JC5624; MUID:97415789; PMID:9268701  
A;Contents: Testis  
A;Accession: JC5624  
A;Molecule type: mRNA  
A;Residues: 1-319 <NAV>  
A;Cross-references: UNIPROT:Q15622; GB:Y10530; NID:92792017; PIDN:CAA71558.1; PID:927920  
R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.  
Submitted to the EMBL Data Library, July 1995  
A;Description: Male germ cells from several mammalian species express a specific reperto  
A;Reference number: S57995  
A;Accession: S58003  
A;Molecule type: mRNA  
A;Residues: 126-282 <VAW>  
A;Cross-references: EMBL:X89677; NID:9902337; PIDN:CAA61824.1; PID:9902338  
C;Genetics:  
A;Map position: 19p13.1  
A;Function:  
A;Description: involved in control of sperm physiology  
C;Superfamily: olfactory receptor OR14  
C;Keywords: G protein-coupled receptor; transmembrane protein  
F;26-48/Domain: transmembrane #status predicted <TM1>  
F;58-79/Domain: transmembrane #status predicted <TM2>

F;101-120/Domain: transmembrane #status predicted <TM3>  
F;140-164/Domain: transmembrane #status predicted <TM4>  
F;197-218/Domain: transmembrane #status predicted <TM5>  
F;237-260/Domain: transmembrane #status predicted <TM6>  
F;272-292/Domain: transmembrane #status predicted <TM7>

Query Match 38.0%; Score 674; DB 2; Length 319;  
Best Local Similarity 45.8%; Pred. No. 3.4e-50;  
Matches 138; Conservative 53; Mismatches 110; Indels 0; Gaps 0;

QY 22 MEIANVSSPEVFLVLLGFSARPSTLVLFIVLVSYFVMSILNGIILVSHTDVHLHTPMY 81  
Db 1 MEGNDQISETFLLGFSQEPGLQFGLFSLWLVTVLGNLLIILATISDSHLHTPMY 60

QY 82 FFLANLSFLDMGFTTSIVPOLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMSY 141  
Db 61 FFLSNLSFADICVTSTTPKLMNIIQTNKVITYIACLMQMYFFILFAGFENFLLSVAY 120

QY 142 DYAAACRPLHYTVIMHPOLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFCE 201  
Db 121 DRFVALCHPLHYTVIMHPOLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFCE 180

QY 202 MPLIMQLACVDTSLNEMMYLASFVFWLPLGLHILVSYGHARAVLKIERSAEGRRKAFNT 261  
Db 181 LNOVIQLACSDSFLNHWIYFTVALLGGGLTGLILYSYSKLISSIIHAISSAQCKYKAFST 240

QY 262 CSSHVAVVSLFYGSIIFMYLOPAKTSHEQKFI--ALFYTVVTPALNPLIYTLRNTSVK 321  
Db 241 CASHLSVSLFYGAILGVYLSAATRNSSSATSVMYTVVTPMLNPFYISLRNKDIKRA 300

QY 322 L 322  
Db 301 L 301

RESULT 10  
S20572  
olfactory receptor - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S20572  
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schifmann, S.; Lefort, A.; Eggerickx, D.; I  
Nature 355, 453-455, 1992  
A;Title: Expression of members of the putative olfactory receptor gene family in mamma  
A;Reference number: S20571; MUID:92131132; PMID:1370859  
A;Accession: S20572  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-314 <PAR>  
A;Cross-references: UNIPROT:P30953; EMBL:X64994; NID:932085; PIDN:CAA46127.1; PID:g32086  
C;Superfamily: olfactory receptor OR14  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 37.8%; Score 672; DB 2; Length 314;  
Best Local Similarity 43.9%; Pred. No. 4.9e-50;  
Matches 133; Conservative 62; Mismatches 104; Indels 4; Gaps 2;

QY 26 NVSSPEVFLVLLGFSARPSTLVLFIVLVSYFVMSILNGIILVSHTDVHLHTPMYFPLA 85  
Db 5 NOTSIDPFLLLGLPIQPEQONLCVALFLAWYLTLLGNLLIILVLRDLSHLHTPMYFLS 64

QY 86 NLSFLDMGFTTSIVPOLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMSYDRIA 145  
Db 65 NLSFDLCFSSVTIPKLLQNNQNDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYV 124

QY 146 AICRPLHYTVIMHPOLCLGLALASWLGGLT--SMVGSTLTMLPLCGNCCIDHFFCEMP 203  
Db 125 AICFPLHYTAIWSPMCLALVALSWV--LTFHAMLHTLMARLCFCADNVIPHFFCDMS 182

QY 204 LIMQLACVDTSLNEMMYLASFVFWLPLGLHILVSYGHARAVLKIERSAEGRRKAFNTCS 263  
Db 193 ALLKLAFSDTRVNEWVIFIMGGLIIVPFLIILGSYARIVSSILKVPSSKGIKAFSTCG 242



Eur. J. Biochem. 225, 1157-1168, 1994  
A:Title: Olfactory receptor proteins. Expression, characterization and partial purification  
A:Reference number: S51356; MID:95045546; PMID:7957207  
A:Accession: S51356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-309 <GAT>  
A:Cross-references: UNIPROT:Q63395; EMBL:X80671; NID:G517365; PIDN:CAA56697.1; PID:G517366  
R:Gat, U.; Nekrasova, E.; Lancel, D.; Natocchin, M.  
submitted to the EMBL Data Library, July 1994  
A:Description: Olfactory receptor proteins: expression, characterization and partial purification  
A:Reference number: S47014  
A:Accession: S47014  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-309 <GAT>  
A:Cross-references: EMBL:X80671; NID:G517365; PIDN:CAA56697.1; PID:G517366  
C:Superfamily: olfactory receptor OR14

Query Match 37.3%; Score 662; DB 1; Length 309;  
Best Local Similarity 44.2%; Pred. No. 3.5e-49;  
Matches 134; Conservative 67; Mismatches 100; Indels 2; Gaps 2;

[illegible]

RESULT 15  
C23701  
olfactory receptor P6 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C:Accession: C23701  
R:Buck, L.; Axel, R.  
Cell 65, 175-187, 1991  
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od  
A:Reference number: A23701; MUID:91191556; PMID:1840504  
A:Accession: C23701  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-311 <BUC>  
A:Cross-references: UNIPROT:P23267; GB:M64378; NID:G205817; PIDN:AAA41741.1; PID:G205818  
C:Superfamily: olfactory receptor OR14  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 37.2%; Score 660; DB 2; Length 311;  
Best Local Similarity 45.2%; Pred. No. 5.2e-49;  
Matches 137; Conservative 53; Mismatches 109; Indels 4; Gaps 2;

**Oy**

26 NVSSPEVFLIGFSARPSLETVLFIIVLSPFWWSILNGIILVSHTDVH--LHTPMYFF 83  
| : | : ||||| : ||| : : ::::| : ::| : |||||  
**Ddb**

8 NLSTGPIIGFGPGPRSMRGLFLLFIWILLTVVGN--LAISLVGAHRCLQTPMYFF 65  
| : | : ||||| : ||| : : ::::| : ::| : |||||

QY	84	LANISFLDMSTTSIVPOLLANLWGPQKTIISYGGCVVQFYISHWLGATECVLLATMSYDR	143
Db	66	LCNLSFLEINFTWETACVPKTLTATPAPRGVVISLAGCATQMFVFSLGCTEYFLLAVMAYDR	125
QY	144	YAAICRPLHYTVINHPOLCIGLALASWLGGLTTSWVGSTLTWMLPLCGNCCIDHFFCEMP	203
Db	126	YLALCLPLRYGGIWTPLGAWRLALGSLWLCGFSAITVPATLIARLSFCGSSRVINHPFCDIS	185
QY	204	LIMOLACVDTSLNEMEMYLASPFVVLPLGLILVSYGHIAVARVLKIRSAEGRKKAFNCTCS	263
Db	186	PWIVLSCTDQVVELVSFGIAFCVILGSCGILTUVSYAVIITIIKIIPSGRGEHRAFTCS	245
QY	264	SHVAVSLFYGSIIEWYLOPAKSTSEHQKFALPFTVVTPALNPLIITLRLNTEVKSALR	323
Db	246	SHLVVLVIWGSTIFLHVRTSVESSDLTKAITVLNTIVTVPVLPNFYITLRNKOVKEALR	305
QY	324	HMV	326
Db	306	RTV	308

Search completed: April 8, 2005, 17:09:17  
Job time : 47 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2005, 17:05:35 ; Search time 140 Seconds  
(without alignments)  
806.279 Million cell updates/sec

Title: US-10-633-894-6  
Perfect score: 1776  
Sequence: 1 MPCMPALPGGLLPQHPT.....ALRMVLENCSSAGKLAQI 340

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_5/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*  
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5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1776	100.0	340	15	US-10-633-894-6
2	1767	99.5	340	9	US-09-886-055-465
3	1767	99.5	340	10	US-09-804-291-465
4	1725	97.1	377	15	US-10-343-650A-536
5	1651	93.0	320	11	US-09-981-566A-28
6	1646	92.7	320	15	US-10-005-041A-28
7	1645	92.6	320	14	US-10-017-161-566
8	1645	92.6	320	15	US-10-292-798-494
9	1640	92.3	319	16	US-10-473-518-39
10	1565	88.1	305	15	US-10-024-212-118
11	1009	56.8	317	17	US-10-774-355A-1895
12	990	55.7	350	9	US-09-886-055-397
13	990	55.7	350	10	US-09-804-291-397

14	990	55.7	350	14	US-10-017-161-20	Sequence 20, Appl
15	990	55.7	350	15	US-10-343-650A-570	Sequence 570, Appl
16	985	55.5	312	10	US-09-795-271-58	Sequence 58, Appl
17	985	55.5	312	10	US-09-907-218-47	Sequence 47, Appl
18	985	55.5	312	10	US-09-907-218-78	Sequence 78, Appl
19	985	55.5	312	10	US-09-912-976-55	Sequence 55, Appl
20	985	55.5	312	10	US-09-912-976-61	Sequence 61, Appl
21	985	55.5	312	10	US-09-965-422-49	Sequence 49, Appl
22	985	55.5	312	11	US-09-981-566A-29	Sequence 29, Appl
23	985	55.5	312	15	US-10-005-041A-95	Sequence 95, Appl
24	985	55.5	312	15	US-10-005-041A-107	Sequence 107, Appl
25	985	55.5	312	10	US-09-965-422-10	Sequence 10, Appl
26	984.5	55.4	309	10	US-09-912-976-16	Sequence 16, Appl
27	984.5	55.4	309	10	US-09-965-422-12	Sequence 12, Appl
28	984.5	55.4	309	14	US-10-032-189-111	Sequence 111, Appl
29	984.5	55.4	309	15	US-10-292-798-38	Sequence 38, Appl
30	984.5	55.4	309	16	US-10-467-252-32	Sequence 32, Appl
31	984	55.4	312	10	US-09-795-271-12	Sequence 12, Appl
32	984	55.4	312	9	US-09-886-055-365	Sequence 365, Appl
33	984	55.4	312	10	US-09-804-291-365	Sequence 365, Appl
34	983	55.3	312	17	US-10-774-355A-1915	Sequence 1915, Appl
35	981	55.2	315	10	US-09-912-976-20	Sequence 20, Appl
36	978	55.1	334	10	US-09-965-422-4	Sequence 4, Appl
37	978	55.1	334	15	US-10-005-041A-32	Sequence 32, Appl
38	977.5	55.0	309	10	US-09-912-976-18	Sequence 18, Appl
39	977	55.0	314	17	US-10-774-355A-1902	Sequence 1902, Appl
40	977	55.0	334	10	US-09-965-422-6	Sequence 6, Appl
41	977	55.0	334	10	US-09-965-422-8	Sequence 8, Appl
42	977	55.0	334	15	US-10-633-894-8	Sequence 8, Appl
43	976	55.0	311	10	US-09-795-271-62	Sequence 62, Appl
44	976	55.0	312	10	US-09-795-271-55	Sequence 55, Appl
45	976	55.0	312	11	US-09-981-566A-30	Sequence 30, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-633-894-6  
; Sequence 6, Application US/10633894  
; Publication No. US20040029232A1  
; GENERAL INFORMATION:  
; APPLICANT: Powers, Scott  
; APPLICANT: Yang, Jianxin  
; APPLICANT: Cutler, Gene  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: No. US20040029232A1e1 G-Protein Coupled Receptors  
; FILE REFERENCE: 018781-004720US  
; CURRENT APPLICATION NUMBER: US/10/633,894  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: US/09/546,986A  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 09/524,730  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-633-894-6

Query Match 100.0%; Score 1776; DB 15; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.5e-156;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPCMPALPGGLLPQHPTMEIANVSSPEVFLGFSARPSETLVFLVLSFYWVSI	60
Db	1	MPCMPALPGGLLPQHPTMEIANVSSPEVFLGFSARPSETLVFLVLSFYWVSI	60
Qy	61	LGNGIILVSHDTHLHTPMYFFLANLSFLDMFTTISIVPQLLANLWGPQKTSYGGCVV	120
Db	61	LGNGIILVSHDTHLHTPMYFFLANLSFLDMFTTISIVPQLLANLWGPQKTSYGGCVV	120

QY 121 QFYISHLWGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
Db 121 QFYISHLWGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
QY 181 STLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
Db 181 STLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLOPAKSTSHQKGFALFYT 300  
Db 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLOPAKSTSHQKGFALFYT 300  
QY 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340  
Db 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340

## RESULT 2

US-09-886-055-465  
; Sequence 465, Application US/09886055  
; Patent No. US20020132273A1  
; GENERAL INFORMATION:  
; APPLICANT: STRYER, LUBERT  
; APPLICANT: ZOZULYA, SERGEY  
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND  
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS  
; FILE REFERENCE: 078003-0277150  
; CURRENT APPLICATION NUMBER: US/09/886,055  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,812  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 522  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 465  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-886-055-465

Query Match 99.5%; Score 1767; DB 9; Length 340;  
Best Local Similarity 99.4%; Pred. No. 1e-155;  
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSTLVLFIVLVSFYMVISI 60  
Db 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSTLVLFIVLVSFYMVISI 60  
QY 61 LCGNIIILVSHDTHLHTPMYFFFLANLSPFLDMSFTTSIVPQLLANLWGPQKTSISYGCVV 120  
Db 61 LCGNIIILVSHDTHLHTPMYFFFLANLSPFLDMSFTTSIVPQLLANLWGPQKTSISYGCVV 120  
QY 121 QFYISHLWGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
Db 121 QFYISHLWGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
QY 181 STLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
Db 181 STLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLOPAKSTSHQKGFALFYT 300  
Db 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLOPAKSTSHQKGFALFYT 300  
QY 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340  
Db 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340

## RESULT 3

US-09-804-291-465  
; Sequence 465, Application US/09804291  
; Publication No. US2003008059A1

; GENERAL INFORMATION:  
; APPLICANT: ZOZULYA, SERGEY  
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME  
; FILE REFERENCE: P 0278005  
; CURRENT APPLICATION NUMBER: US/09/804,291  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: 60/188,914  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/192,033  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/198,474  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/199,335  
; PRIOR FILING DATE: 2000-04-24  
; PRIOR APPLICATION NUMBER: 60/207,702  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/213,849  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/226,534  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 60/230,732  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/266,862  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 465  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-804-291-465

Query Match 99.5%; Score 1767; DB 10; Length 340;  
Best Local Similarity 99.4%; Pred. No. 1e-155;  
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSTLVLFIVLVSFYMVISI 60  
Db 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLVLLGFSARPSTLVLFIVLVSFYMVISI 60  
QY 61 LCGNIIILVSHDTHLHTPMYFFFLANLSPFLDMSFTTSIVPQLLANLWGPQKTSISYGCVV 120  
Db 61 LCGNIIILVSHDTHLHTPMYFFFLANLSPFLDMSFTTSIVPQLLANLWGPQKTSISYGCVV 120  
QY 121 QFYISHLWGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
Db 121 QFYISHLWGATECVLLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVG 180  
QY 181 STLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
Db 181 STLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVVLPLGLILVSYG 240  
QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLOPAKSTSHQKGFALFYT 300  
Db 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLOPAKSTSHQKGFALFYT 300  
QY 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340  
Db 301 VVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKLAQI 340

## RESULT 4

US-10-343-650A-596  
; Sequence 596, Application US/10343650A  
; Publication No. US20040067499A1  
; GENERAL INFORMATION:  
; APPLICANT: HAGA, TATSUYA  
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: 31671-186347  
; CURRENT APPLICATION NUMBER: US/10/343,650A  
; CURRENT FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: JP 2000/237818  
; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: JP 2001/34434  
; PRIOR FILING DATE: 2001-02-13  
; NUMBER OF SEQ ID NOS: 694  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 596  
; LENGTH: 377  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (10)..(43)  
; OTHER INFORMATION: Variable amino acid  
US-10-343-650A-596

Query Match 97.1%; Score 1725; DB 15; Length 377;  
Best Local Similarity 99.4%; Pred. No. 9.4e-152;  
Matches 332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 ALPTGGLPHQHTMMEIANVSSPEVFLGFSARPSLETVLFVWLSFYMVSLGNGII 66  
DB 44 ALPTGGLPHQHTMMEIANVSSPEVFLGFSARPSLETVLFVWLSFYMVSLGNGII 103  
QY 67 ILVSHDTHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISH 126  
DB 104 ILVSHDTHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISH 163  
QY 127 WLGAATECVLLATMSYDYAAICRPLHVTVMHPOLCIGLALASWLGSLTSMVGSSTLTM 186  
DB 164 WLGAATECVLLATMSYDYAAICRPLHVTVMHPOLCIGLALASWLGSLTSMVGSSTLTM 223  
QY 187 LPLCGNCCIDHFCCEMPLIQACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAARV 246  
DB 224 LPLCGNCCIDHFCCEMPLIQACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAARV 283  
QY 247 LKRSAGRRKAFNCTSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALFYTVVTPAL 306  
DB 284 LKRSAGRRKAFNCTSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALFYTVVTPAL 343  
QY 307 NPLIYTLRNTSEVKSALRHMVLENCSSAGKLAQI 340  
DB 344 NPLIYTLRNTSEVKSALRHMVLENCSSAGKLAQI 377

RESULT 5  
US-09-981-566A-28  
; Sequence 28, Application US/09981566A  
; Publication No. US20040005656A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda et al.  
; TITLE OF INVENTION: No. US20040005656A1el GPCR-like Proteins and Nucleic Acids Encod  
; FILE REFERENCE: 21402-163  
; CURRENT APPLICATION NUMBER: US/09/981.566A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 60/240,704  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/262,159  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/263,340  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/264,118  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/308,203  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/243,497  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: 60/244,542  
; PRIOR FILING DATE: 2000-10-31  
; PRIOR APPLICATION NUMBER: 60/269,031  
; PRIOR FILING DATE: 2001-02-15  
; PRIOR APPLICATION NUMBER: 60/245,484  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: 60/255,017

; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/263,216  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/268,225  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 209  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-981-566A-28

Query Match 93.0%; Score 1651; DB 11; Length 320;  
Best Local Similarity 99.7%; Pred. No. 5.8e-145;  
Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 21 MMEIANVSSPEVFLGFSARPSLETVLFVWLSFYMVSLGNGIIILVSHDTHLHTPM 80  
DB 1 MMEIANVSSPEVFLGFSARPSLETVLFVWLSFYMVSLGNGIIILVSHDTHLHTPM 60  
QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMS 140  
DB 61 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMS 120  
QY 141 YDYAAICRPLHVTVMHPOLCIGLALASWLGSLTSMVGSSTLTMPLCGNCCIDHFFC 200  
DB 121 YDYAAICRPLHVTVMHPOLCIGLALASWLGSLTSMVGSSTLTMPLCGNCCIDHFFC 180  
QY 201 EMPLIQACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAARVLIKRSAGRRKAFN 260  
DB 181 EMPLIQACVDTSLNEMEMYLASFVFLPLGLILVSYGHIAARVLIKRSAGRRKAFN 240  
QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALFYTVVTPALNPLYTLRNTSEVKS 320  
DB 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALFYTVVTPALNPLYTLRNTSEVKS 300  
QY 321 ALRHMVLENCSSAGKLAQI 340  
DB 301 ALRHMVLENCSSAGKLAQI 320

RESULT 6  
US-10-005-041A-28  
; Sequence 28, Application US/10005041A  
; Publication No. US20030232331A1  
; GENERAL INFORMATION:  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Pedigaru, Muralidhara  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Gilbert, Jennifer A  
; APPLICANT: Mayotte, Jane E  
; APPLICANT: Baumgartner, Jason C  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Vernet, Corine AM  
; APPLICANT: Dickinson, Kevin S  
; APPLICANT: Ballinger, Robert A  
; APPLICANT: Wolenc, Adam R  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: MacDougall, John R  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J  
; APPLICANT: Gunther, Erik  
; APPLICANT: Gerlach, Valerie  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-215  
; CURRENT APPLICATION NUMBER: US/10/005,041A  
; CURRENT FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/251,459  
; PRIOR FILING DATE: 2000-12-05

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; PRIOR APPLICATION NUMBER: 60/259,007
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-041A-28

Query Match          92.7%; Score 1646; DB 15; Length 320;
Best Local Similarity 99.4%; Pred. No. 2.1e-144;
Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 21 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 80
DB 1 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 60

QY 81 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 140
DB 61 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 120

QY 141 YDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 200
DB 121 YDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 180

QY 201 EMPLIMOLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRRAFN 260
DB 181 EMPLIMOLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRRAFN 240

QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYVTVTPALNPLIYTLRNTEVKS 320
DB 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYVTVTPALNPLIYTLRNTEVKS 300

QY 321 ALRHMVLENCSSAGKLAQI 340
DB 301 ALRHMVLENCSSAGKLAQI 320

RESULT 7
US-10-017-161-566
; Sequence 566, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 566
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-566

Query Match          92.6%; Score 1645; DB 14; Length 320;
Best Local Similarity 99.4%; Pred. No. 2.1e-144;
Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 80
DB 1 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 60

QY 81 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 140
DB 61 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 120

QY 141 YDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 200
DB 121 YDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 180

QY 201 EMPLIMOLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRRAFN 260
DB 181 EMPLIMOLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRRAFN 240

QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYVTVTPALNPLIYTLRNTEVKS 320
DB 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYVTVTPALNPLIYTLRNTEVKS 300

QY 321 ALRHMVLENCSSAGKLAQI 340
DB 301 ALRHMVLENCSSAGKLAQI 320

RESULT 8
US-10-292-798-494
; Sequence 494, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-494

Query Match          92.6%; Score 1645; DB 15; Length 320;
Best Local Similarity 99.4%; Pred. No. 2.1e-144;
Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 80
DB 1 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 60

QY 81 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 140
DB 61 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 120

QY 141 YDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 200
DB 121 YDRAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVVGSTLTMLPLCGNCCIDHFFC 180

QY 201 EMPLIMOLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRRAFN 260
DB 181 EMPLIMOLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAARAVLKIRSAEGRRAFN 240

QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYVTVTPALNPLIYTLRNTEVKS 320
DB 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYVTVTPALNPLIYTLRNTEVKS 300

QY 321 ALRHMVLENCSSAGKLAQI 340
DB 301 ALRHMVLENCSSAGKLAQI 320

RESULT 9
US-10-017-161-566
; Sequence 566, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 566
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-566

Query Match          92.6%; Score 1645; DB 14; Length 320;
Best Local Similarity 99.4%; Pred. No. 2.1e-144;
Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 80
DB 1 MMEIANVSSPEVFLVGLGFSARPSLETVLFIIVLSFYVMSILNGIIILVSHDTHLHTPM 60

QY 81 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 140
DB 61 YFLANLSFLDMSFTTSIVPOLLANLWGPKTISYGGCVQVFIYSHWLGATECVLLATMS 120
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US-10-473-518-39  
; Sequence 39, Application US/10473518  
; Publication No. US20040138416A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION  
; APPLICANT: THORNTON, Michael B.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: RICHARDSON, Thomas W.  
; APPLICANT: SWARNAKAR, Anita  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: ELIOTT, Vicki S.  
; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: AU-YOUNG, Janice K.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: KHAN, Farrah A.  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: LU, Yan  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: WALSH, Roderick T.  
; APPLICANT: YUE, Henry  
; APPLICANT: BURFORD, Neil  
; APPLICANT: GRAUL, Richard C.  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PF-0933 USN  
; CURRENT APPLICATION NUMBER: US/10/473,518  
; CURRENT FILING DATE: 2003-09-30  
; PRIOR APPLICATION NUMBER: PCT/US02/09923  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/287,266  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/285,336  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: US 60/283,714  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/280,683  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: PERL Program  
; SEQ ID NO 39  
; LENGTH: 319  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; FEATURE:  
; OTHER INFORMATION: Incyte ID No: 7476679CD1  
US-10-473-518-39

Query Match 92.3%; Score 1640; DB 16; Length 319;  
Best Local Similarity 99.4%; Pred. No. 6.1e-144;  
Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 22 MEATNVSSPEFVLLGFSAPSETVLFIVVLSFYMVSIILNGIILVSVHTDVHLHTPMY 81  
Db 1 MEATNVSSPEFVLLGFSAPSETVLFIVVLSFYMVSIILNGIILVSVHTDVHLHTPMY 60  
Qy 82 FFLANLSFLDMSFTTSVLPOLLANLWGPQKTSYGGCVQVQFYISHWLGATECVLLATMSY 141  
Db 61 FFLANLFLDMSFTTSVLPOLLANLWGPQKTSYGGCVQVQFYISHWLGATECVLLATMSY 120  
Qy 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMVSTLTMLPLCGNCCIDHFFCE 201  
Db 121 DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMVSTLTMLPLCGNCCIDHFFCE 180  
Qy 202 MPLIMQLACVDTSLNEMENYLASFVFLPLGLILVSYGHIAARAVLKIRSAEGRKAFNT 261

Db 181 MPLIMQLACVDTSLNEMENYLASFVFLPLGLILVSYGHIAARAVLKIRSAEGRKAFNT 240  
Qy 262 CSSHVAVVSIFYGSIIFMYLQPAKSTSHQCKFTALFYTVVTPALNPLIYTLRNTVEKSA 321  
Db 241 CSSHVAVVSIFYGSIIFMYLQPAKSTSHQCKFTALFYTVVTPALNPLIYTLRNTVEKSA 300  
Qy 322 LRHMVLENCSSAGKLAQI 340  
Db 301 LRHMVLENCSSAGKLAQI 319  
RESULT 10  
US-10-024-212-118  
; Sequence 118, Application US/10024212  
; Publication No. US2003023232A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Kekuda, Rameesh  
; APPLICANT: Li, Li  
; APPLICANT: Ballinger, Robert A  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Colman, Steven D  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Stone, David J  
; APPLICANT: Scioere, Paul  
; APPLICANT: MacDougall, John R  
; APPLICANT: Gunther, Erik  
; APPLICANT: Peyman, John A  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Anderson, David W  
; APPLICANT: Wolenc, Adam R  
; TITLE OF INVENTION: No. US2003023232A1e1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-224AA  
; CURRENT APPLICATION NUMBER: US/10/024,212  
; CURRENT FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/256,635  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/259,743  
; PRIOR FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: 60/299,327  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: 60/261,498  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/263,689  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/267,464  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/271,021  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/275,946  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/278,150  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/285,718  
; PRIOR FILING DATE: 2001-04-23  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 476  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 118  
; LENGTH: 305  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-212-118

```
Query Match      88.1%; Score 1565; DB 15; Length 305;
Best Local Similarity 99.3%; Pred. No. 5.3e-137;
Matches 303; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 MEANVSSPEVFLVGLGFSARPSLETFLVFLVLSFYVMSILNGIILVSHHTDVHLHTPMY 81
DB 1 MEANVSSPEVFLVGLGFSARPSLETFLVFLVLSFYVMSILNGIILVSHHTDVHLHTPMY 60

QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGAECVLLATMSY 141
DB 61 FFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGAECVLLATMSY 120

QY 142 DRYAAICRPLHTVIMHPOLCIGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFCE 201
DB 121 DRYAAICRPLHTVIMHPOLCIGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFCE 180

QY 202 MPLIMQLACVDTSLNEMEMYLASFVFLVPLGLIILVSYGHIAVARVLRKIRSAEGRKAFNT 261
DB 181 MPLIMQLACVDTSLNEMEMYLASFVFLVPLGLIILVSYGHIAVARVLRKIRSAEGRKAFNT 240

QY 262 CSHSHVAVSLFYGSIIFMYLOPAKSTSHQKGFIALFYVTVTPALNPLIYTLRNTKVA 321
DB 241 CSHSHVAVSLFYGSIIFMYLOPAKSTSHQKGFIALFYVTVTPALNPLIYTLRNTKVA 300

QY 322 LRHMV 326
DB 301 LRHMV 305

RESULT 11
US-10-774-355A-1895
; Sequence 1895, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774.355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1895
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-774-355A-1895

Query Match      56.8%; Score 1009; DB 17; Length 317;
Best Local Similarity 61.9%; Pred. No. 2.5e-85;
Matches 190; Conservative 51; Mismatches 64; Indels 2; Gaps 2;

QY 21 MMEANVSSPEVFLVGLGFSARPSLETFLVFLVLSFYVMSILNGIILVSHHTDVHLHTPM 80
DB 5 VMKEKNTSSPEGFLVGLGFSARPSLETFLVFLVLSFYVMSILNGIILVSHHTDVHLHTPM 64

QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGAECVLLATMSY 140
DB 65 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGAECVLLATMSY 124

QY 141 YDRIAAICRPLHTVIMHPOLCIGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFCE 200
DB 125 YDRIAAICRPLHTVIMHPOLCIGLALASWLGGLTSMVGSTLTMLPLCGNCCIDHFFCE 184

QY 201 EMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLIILVSYGHIAVARVLRKIRSAEGRKAF 259
DB 201 EMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLIILVSYGHIAVARVLRKIRSAEGRKAF 259

Db 185 EMPALIGMACVDVTWALEALAFALAIPT-ILAPLILILISYGTARAVRIKSAAGRRKAF 243
QY 260 NTCSSHVAVSLFYGSIIFMYLOPAKSTSHQKGFIALFYVTVTPALNPLIYTLRNTKVA 319
DB 244 NTCSSHLIVVLSFYGTIIYMYLOPANTYSQDQKFLTFVTIVTPSNPLIYTLRNDVK 303
QY 320 SALRHV 326
DB 304 EAVKVL 310

RESULT 12
US-09-886-055-397
; Sequence 397, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LOBERT
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 397
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-397

Query Match      55.7%; Score 990; DB 9; Length 350;
Best Local Similarity 54.8%; Pred. No. 1.6e-83;
Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;

QY 3 CMPC-----ALPTGGLPHPHQHTMMEIANVSPSEVFLVGLGFSARPSLETFLVFLVLS 54
DB 24 CFGCTHSIPALGADPPGG-----MGLGNESLMDFILLGFSDPHLEAVLFVFLV 74

QY 55 FYMVSILNGIILVSHHTDVHLHTPMYFLANLSFLDMSFTTSIVPQLLANLWGPQKTS 114
DB 75 FYLLTVGNFTIIISYLDPPHLPHTPMYFLSLSLDDICFTSLAPQTLVNLQRPKKTIT 134

QY 115 YGCVVQFYISHWLGAECVLLATMSYDRIAAICRPLHTVIMHPOLCIGLALASWLGGL 174
DB 135 YGCVVQFYISHWLGAECVLLATMSYDRIAAICRPLHTVIMHPOLCIGLALASWLGGL 194

QY 175 TTSVMVGSTLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGL 234
DB 195 ASSLIHATFTLQLPLCGNHRLDHFICEVPAALLKLACVDTTNNELVLFVSVLFFVVPAL 254

QY 235 IIVSYGHIAVARVLRKIRSAEGRKAFNTCSSHVAVSLFYGSIIFMYLOPAKSTSHQKGF 294
DB 255 ISISYGHIAVARVLRKIRSAEGRKAFNTCSSHVAVSLFYGSIIFMYLOPAKSTSHQKGF 314

QY 295 IALFYTVTPALNPLIYTLRNTKVAALRHVLENCSSAGKL 337
DB 315 ISLFYTVTPALNPLIYTLRNTKVAALRHVLENCSSAGKL 350

RESULT 13
US-09-804-291-397
; Sequence 397, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
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; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 397
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-397

Query Match      55.7%; Score 990; DB 10; Length 350;
Best Local Similarity 54.8%; Pred. No. 1.6e-83;
Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;

Qy      3 CMPC-----ALPTGGLLPHQHTMWEIANVSSPEVFLVLLGFSARPSLETVLFIIVVLS 54
Db      24 CFGCTHSIPALGADPPGG-----MGLGNSSLMDFIILLGFSDPHRLPRLVAVLFFVFLF 74

Qy      55 FYMVSILNGGIIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTI 114
Db      75 FYLLTLVGNFTIIIIISYLDPLHTPMYFFLSNLSLLDICTTSLAPQTLVNLQRPKKTIT 134

Qy      115 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 174
Db      135 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 194

Qy      175 TTSVMGSLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGL 234
Db      195 ASSLIHATFTLQLPLCGNHRDLDFICEVPALLKACVDTTNNELVLFVVSFLFVVIIPAL 254

Qy      235 ILVSYGHIARAVLKIRSAEGRKAFNCTSSHVAVVSFLFYGSIIPMYLQPAKSTSHQCKF 294
Db      255 ISISYGFITQAVLRKISVEARHKAFSTCSSHLTVIIIFYGTIIIVYIQLPSDSYAQDQKF 314

Qy      295 IALPYTVVTPALNPLIYTLRNTVEKSAHRHMLVLENCSSAGKL 337
Db      315 ISLFYTWVTPNLPIIYTLRNMKMEALRKL-----SGKL 350

RESULT 14
US-10-017-161-20
; Sequence 20, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUNA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 350

Query Match      55.7%; Score 990; DB 10; Length 350;
Best Local Similarity 54.8%; Pred. No. 1.6e-83;
Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;

Qy      3 CMPC-----ALPTGGLLPHQHTMWEIANVSSPEVFLVLLGFSARPSLETVLFIIVVLS 54
Db      24 CFGCTHSIPALGADPPGG-----MGLGNSSLMDFIILLGFSDPHRLPRLVAVLFFVFLF 74

Qy      55 FYMVSILNGGIIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTI 114
Db      75 FYLLTLVGNFTIIIIISYLDPLHTPMYFFLSNLSLLDICTTSLAPQTLVNLQRPKKTIT 134

Qy      115 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 174
Db      135 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 194

Qy      175 TTSVMGSLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGL 234
Db      195 ASSLIHATFTLQLPLCGNHRDLDFICEVPALLKACVDTTNNELVLFVVSFLFVVIIPAL 254

Qy      235 ILVSYGHIARAVLKIRSAEGRKAFNCTSSHVAVVSFLFYGSIIPMYLQPAKSTSHQCKF 294
Db      255 ISISYGFITQAVLRKISVEARHKAFSTCSSHLTVIIIFYGTIIIVYIQLPSDSYAQDQKF 314

Qy      295 IALPYTVVTPALNPLIYTLRNTVEKSAHRHMLVLENCSSAGKL 337
Db      315 ISLFYTWVTPNLPIIYTLRNMKMEALRKL-----SGKL 350

RESULT 15
US-10-343-650A-570
; Sequence 570, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 570
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-570

Query Match      55.7%; Score 990; DB 15; Length 350;
Best Local Similarity 54.8%; Pred. No. 1.6e-83;
Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;

Qy      3 CMPC-----ALPTGGLLPHQHTMWEIANVSSPEVFLVLLGFSARPSLETVLFIIVVLS 54
Db      24 CFGCTHSIPALGADPPGG-----MGLGNSSLMDFIILLGFSDPHRLPRLVAVLFFVFLF 74

Qy      55 FYMVSILNGGIIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTI 114
Db      75 FYLLTLVGNFTIIIIISYLDPLHTPMYFFLSNLSLLDICTTSLAPQTLVNLQRPKKTIT 134

Qy      115 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 174
Db      135 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 194

Qy      175 TTSVMGSLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGL 234
Db      195 ASSLIHATFTLQLPLCGNHRDLDFICEVPALLKACVDTTNNELVLFVVSFLFVVIIPAL 254

Qy      235 ILVSYGHIARAVLKIRSAEGRKAFNCTSSHVAVVSFLFYGSIIPMYLQPAKSTSHQCKF 294
Db      255 ISISYGFITQAVLRKISVEARHKAFSTCSSHLTVIIIFYGTIIIVYIQLPSDSYAQDQKF 314

Qy      295 IALPYTVVTPALNPLIYTLRNTVEKSAHRHMLVLENCSSAGKL 337
Db      315 ISLFYTWVTPNLPIIYTLRNMKMEALRKL-----SGKL 350
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-20

Query Match      55.7%; Score 990; DB 14; Length 350;
Best Local Similarity 54.8%; Pred. No. 1.6e-83;
Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;

Qy      3 CMPC-----ALPTGGLLPHQHTMWEIANVSSPEVFLVLLGFSARPSLETVLFIIVVLS 54
Db      24 CFGCTHSIPALGADPPGG-----MGLGNSSLMDFIILLGFSDPHRLPRLVAVLFFVFLF 74

Qy      55 FYMVSILNGGIIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTI 114
Db      75 FYLLTLVGNFTIIIIISYLDPLHTPMYFFLSNLSLLDICTTSLAPQTLVNLQRPKKTIT 134

Qy      115 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 174
Db      135 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 194

Qy      175 TTSVMGSLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGL 234
Db      195 ASSLIHATFTLQLPLCGNHRDLDFICEVPALLKACVDTTNNELVLFVVSFLFVVIIPAL 254

Qy      235 ILVSYGHIARAVLKIRSAEGRKAFNCTSSHVAVVSFLFYGSIIPMYLQPAKSTSHQCKF 294
Db      255 ISISYGFITQAVLRKISVEARHKAFSTCSSHLTVIIIFYGTIIIVYIQLPSDSYAQDQKF 314

Qy      295 IALPYTVVTPALNPLIYTLRNTVEKSAHRHMLVLENCSSAGKL 337
Db      315 ISLFYTWVTPNLPIIYTLRNMKMEALRKL-----SGKL 350

RESULT 15
US-10-343-650A-570
; Sequence 570, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 570
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-570

Query Match      55.7%; Score 990; DB 15; Length 350;
Best Local Similarity 54.8%; Pred. No. 1.6e-83;
Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;

Qy      3 CMPC-----ALPTGGLLPHQHTMWEIANVSSPEVFLVLLGFSARPSLETVLFIIVVLS 54
Db      24 CFGCTHSIPALGADPPGG-----MGLGNSSLMDFIILLGFSDPHRLPRLVAVLFFVFLF 74

Qy      55 FYMVSILNGGIIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTI 114
Db      75 FYLLTLVGNFTIIIIISYLDPLHTPMYFFLSNLSLLDICTTSLAPQTLVNLQRPKKTIT 134

Qy      115 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 174
Db      135 YGCVVQFYISHWLGATECVLLATMSYDRVAACRPLHYTVIMHPQCLGLALASWLGGL 194

Qy      175 TTSVMGSLTMLLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGL 234
Db      195 ASSLIHATFTLQLPLCGNHRDLDFICEVPALLKACVDTTNNELVLFVVSFLFVVIIPAL 254

Qy      235 ILVSYGHIARAVLKIRSAEGRKAFNCTSSHVAVVSFLFYGSIIPMYLQPAKSTSHQCKF 294
Db      255 ISISYGFITQAVLRKISVEARHKAFSTCSSHLTVIIIFYGTIIIVYIQLPSDSYAQDQKF 314

Qy      295 IALPYTVVTPALNPLIYTLRNTVEKSAHRHMLVLENCSSAGKL 337
Db      315 ISLFYTWVTPNLPIIYTLRNMKMEALRKL-----SGKL 350
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Db 195 ASSLIHATFTLQLPLCGNHRLDHFICEVPALLKLACVDTTVELVLFVVSULFVVIPPAL 254  
Qy 235 ILVSYGHIARAVLKIIRSAEGRKAFNTCSSHVAVVSLFYGSIIIFMYLQPAKSTSHQCKF 294  
Db 255 ISISYGFITQAVLRIKSVEARHKAFSTCSSLTVVVIIFYGTIIYVYLQPSDSYAQDQCKF 314  
Qy 295 IALFYTVVTPALNPLIYTLRNTVEKSLRHMVLENCSSAGKL 337  
Db 315 ISLFYTMVTPINPIIYTLRNMKBALUKLL-----SGKL 350

Search completed: April 8, 2005, 17:15:42  
Job time : 142 secs